

## STIC-Biotech/ChemLib

55886

**From:** Davis, Minh-Tam  
**Sent:** Monday, December 03, 2001 9:51 AM  
**To:** STIC-Biotech/ChemLib  
**Subject:** RE: Search request for 09/583848

Please use the grandparent cases 08/967727 or 08/037230.  
Thanks

-----Original Message-----

**From:** STIC-Biotech/ChemLib  
**Sent:** Wednesday, November 21, 2001 11:57 AM  
**To:** Davis, Minh-Tam  
**Subject:** RE: Search request for 09/583848

Unfortunately the Parent Case has no CRF either.

Thank you.

-----Original Message-----

**From:** Davis, Minh-Tam  
**Sent:** Wednesday, November 21, 2001 11:22 AM  
**To:** STIC-Biotech/ChemLib  
**Subject:** RE: Search request for 09/583848

Please note that in the request, I asked to use the parent case 09/404026 to search for this case.  
Tam

-----Original Message-----

**From:** STIC-Biotech/ChemLib  
**Sent:** Wednesday, November 21, 2001 11:21 AM  
**To:** Davis, Minh-Tam  
**Subject:** RE: Search request for 09/583848

We are unable to process this search because there is a problem with the CRF data for this case. If there is a related case that should be used, please let us know. **We cannot process this request until valid data is available.** Please contact STIC/Biotech.

Biotech/Chem STIC  
308-4478

-----Original Message-----

**From:** Davis, Minh-Tam  
**Sent:** Wednesday, November 21, 2001 10:35 AM  
**To:** STIC-Biotech/ChemLib  
**Subject:** Search request for 09/583848

Please search in commercial database and in issued patent files:

1) SEQ ID NO:18.

2) Please search against the parent cases PCT/US92/04354, 07/807043, 07/764364, 07/728838, 07/705702 for priority date determination.

Please use the parent case 09/404026 to search for this case.

RECEIVED  
DEC - 3 2001  
(STIC)

error in continuity  
title not in biotech  
no CRF  
5342774

Searcher: D. Schuerber  
Phone: 308-4292  
Location: CM1 12C14  
Date Picked Up: \_\_\_\_\_  
Date Completed: 12/10  
Searcher Prep/Review: 8  
Clerical: \_\_\_\_\_  
Online time: 16

## TYPE OF SEARCH:

NA Sequences: 3  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

## VENDOR/COST(where applic.)

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: Compugen IgFastDB  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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Thank you  
MINH TAM DAVIS  
ART UNIT 1642, ROOM 8A01, MB 8E12  
305-2008

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:

NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST(where applic.)

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 4, 2001, 07:46:17 ; Search time 1159.37 Seconds  
(without alignments)  
2085.443 Million cell updates/sec

Title: US-08-037-230D-18  
Perfect score: 225  
Sequence: 1 TATTTCCTTCTGTGATCTT.....CGGACTGTGCCCTGAGGAG 225

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 11351937 seqs, 5372889281 residues  
Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estfun:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estom:\*  
5: em\_estpl:\*  
6: em\_estba:\*  
7: em\_estro:\*  
8: em\_estov:\*  
9: em\_hic:\*  
10: gb\_est1:\*  
11: gb\_est2:\*  
12: gb\_hic:\*  
13: gb\_gss:\*  
14: em\_gss\_fun:\*  
15: em\_gss\_hum:\*  
16: em\_gss\_inv:\*  
17: em\_gss\_pln:\*  
18: em\_gss\_pro:\*  
19: em\_gss\_rod:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	220.2	97.9	563	11	BG477228
2	220.2	97.9	776	11	BG476912
3	220.2	97.9	876	11	BF792356
4	220.2	97.9	878	11	BG397171
5	220.2	97.9	886	11	BG476078
6	213.8	95.0	623	11	BF793889
7	213.8	95.0	686	11	BG575715
8	213.8	95.0	704	11	B1090658
9	213.8	95.0	769	11	BG765526
10	202.6	90.0	934	11	BG280738
11	201.4	89.5	795	10	BE541476
12	196.8	87.5	590	11	BE897495

13	196.8	87.5	680	10	BE563063
14	196.4	87.3	768	11	BI086876
15	196	87.1	767	11	BI092532
16	195.2	86.8	1089	11	BG029985
17	194	86.2	707	11	BG760839
18	193.6	86.0	484	11	BF970108
19	193.6	86.0	784	11	BF793468
20	178.8	79.5	845	11	BG481937
21	176.8	78.6	894	11	BG765817
22	165.4	73.5	810	10	AL526639
23	164.6	73.2	816	11	BI086919
24	163.4	72.6	797	11	BI087493
25	162.8	72.4	929	11	BE896896
26	159.6	70.9	962	11	BG116297
27	159.6	70.9	1050	11	BG024106
28	156.4	69.5	956	11	BE900736
29	154.8	68.8	876	11	BE795782
30	153.2	68.1	929	10	BE275276
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33	147.6	65.6	922	11	BG115115
34	147.6	65.6	946	11	BF983819
35	146	64.9	948	10	AL562721
36	141.8	63.0	820	11	BG481340
37	138.6	61.6	1109	11	BG333682
38	138.2	61.4	597	10	BE281072
39	134.2	59.6	828	11	BG479591
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41	131.2	58.3	822	11	BE898065
42	130.8	58.1	950	10	BE541026
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44	127.2	56.5	821	11	BG177776
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ALIGNMENTS

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LOCUS 602524237F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:4642641 5',  
DEFINITION mRNA sequence.  
ACCESSION BG477228.1 GI:13409507  
VERSION BG477228  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 563)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: ATCC/DCTD/BTP  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LNCM411 row: i column: 10  
High quality sequence stop: 499.  
Location/Qualifiers  
1. .563  
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Best Local Similarity 98.7%; Pred. No. 1.3e-47; Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
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QY	121	TCCTAGATGGCTGCTGGGTGACATCAGATCATGCCAGGACGGCTTCCTTGATAATC	180						
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LOCUS 602434130F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4552086 5',									
DEFINITION mRNA sequence.									
ACCESSION BG397171									
VERSION BG397171.1 GI:13290619									
KEYWORDS EST.									
SOURCE human.									
ORGANISM Homo sapiens									
REFERENCE 1 (bases 1 to 878)									
AUTHORS NIH-MGC http://mgc.nci.nih.gov/									
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)									
JOURNAL Unpublished (1999)									
COMMENT Contact: Robert Strausberg, Ph.D.									
Email: cgapbs-r@mail.nih.gov									
Tissue Procurement: ATCC/DCTD/DTP									
CDNA Library Preparation: Ling Hong/Rubin Laboratory									
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)									
DNA Sequencing by: Incyte Genomics, Inc.									
Clone distribution: MGC clone distribution information can be									
found through the I.M.A.G.E. Consortium/LLNL at:									
http://image.llnl.gov									
Plate: LLCMI247 row: 1 column: 07									
High quality sequence stop: 866.									
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1. .878									
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/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:									
EcoRI; cDNA made by oligo-dT priming. Directionally									
cloned into EcoRI/XhoI sites using the following 5'									
adaptor: GGCACGAG(G). Size-selected >500bp for average									
insert size 1.8kb. Library constructed by Ling Hong in									
the laboratory of Gerald M. Rubin (University of									
California, Berkeley) using ZAP-cDNA synthesis kit									
(Stratagene) and Superscript II RT (Life Technologies)."									
BASE COUNT 197 a 214 c 262 g 205 t									
ORIGIN									
Query Match 97.9%; Score 220.2; DB 11; Length 878;									
Best Local Similarity 98.7%; Pred. No. 1.3e-47;									
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
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Db	190	TACTTCTTCCCTGTGATCTTCAGCAAGCTTCGGATTCCTTGGCAGCTGGTCTTTGGCATC	249						
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Db	310	TCCTAGATGGCTGCTGGGTGACATCAGATCATGCCAGGACGGCTTCCTTGATAATC	369						
QY	181	ATCCTGGCCATATCCCAAGAGAGGGCGACTGTGCCCTCAGGAG	225						
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LOCUS 602520963F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4639670 5',									
DEFINITION mRNA sequence.									
ACCESSION BG476078									
VERSION BG476078.1 GI:13408357									
KEYWORDS EST.									
SOURCE human.									
ORGANISM Homo sapiens									
REFERENCE 1 (bases 1 to 886)									
AUTHORS NIH-MGC http://mgc.nci.nih.gov/									
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)									
JOURNAL Unpublished (1999)									
COMMENT Contact: Robert Strausberg, Ph.D.									
Email: cgapbs-r@mail.nih.gov									
Tissue Procurement: ATCC/DCTD/DTP									
CDNA Library Preparation: Ling Hong/Rubin Laboratory									
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)									
DNA Sequencing by: Incyte Genomics, Inc.									
Clone distribution: MGC clone distribution information can be									
found through the I.M.A.G.E. Consortium/LLNL at:									
http://image.llnl.gov									
Plate: LLCMI403 row: m column: 15									
High quality sequence stop: 730.									
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/lab_host="DH10B (phage-resistant)"									
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EcoRI; cDNA made by oligo-dT priming. Directionally									
cloned into EcoRI/XhoI sites using the following 5'									
adaptor: GGCACGAG(G). Size-selected >500bp for average									
insert size 1.8kb. Library constructed by Ling Hong in									
the laboratory of Gerald M. Rubin (University of									
California, Berkeley) using ZAP-cDNA synthesis kit									
(Stratagene) and Superscript II RT (Life Technologies)."									
BASE COUNT 183 a 231 c 262 g 210 t									
ORIGIN									
Query Match 97.9%; Score 220.2; DB 11; Length 886;									
Best Local Similarity 98.7%; Pred. No. 1.3e-47;									
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
QY	1	TATTTCTTCCCTGTGATCTTCAGCAAGCTTCGGATTCCTTGGCAGCTGGTCTTTGGCATC	60						
Db	94	TACTTCTTCCCTGTGATCTTCAGCAAGCTTCGGATTCCTTGGCAGCTGGTCTTTGGCATC	153						
QY	61	GAGCTGATGAAGTGGACCCCATCGGCCACGCTGTACATCTTTGCCACCTGCCCTGGGCCCTC	120						
Db	154	GAGCTGATGAAGTGGACCCCATCGGCCACGCTGTACATCTTTGCCACCTGCCCTGGGCCCTC	213						

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QY 121 TCCTACGATGGCTCTCTGGGTGACAAATCAGATCATGCCCCAGACAGGCTTCTCTGATAATC 180
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QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
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Db 274 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 318
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RESULT 6
LOCUS BF793889 623 bp mRNA EST 12-JAN-2001
DEFINITION 60225285F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4347380 5',
mRNA sequence.
ACCESSION BF793889
VERSION BF793889.1 GI:12098943
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 623)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9970 row: j column: 21
High quality sequence stop: 622.
Location/Qualifiers
1. 623
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/tissue_type="adrenal cortex carcinoma, cell line"
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/note="Organ: adrenal gland; Vector: pCMV-Sport6; Site_1:
NotI; Site_2: SalI; Cloned unidirectionally; oligo-dr
primed. Average insert size 1.229 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 136 a 173 c 177 g 137 t
ORIGIN

Query Match 95.0%; Score 213.8; DB 11; Length 623;
Best Local Similarity 96.9%; Pred. No. 5.7e-46;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCTCGAGTGGTCTTTGGCATC 60
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QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACTGCTGGGCCTC 120
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Db 386 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACTGCTGGGCCTC 445
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QY 121 TCCTACCATGGCTGCTGGGTGACAAATCAGATCATGCCCCAGACAGGCTTCTCTGATAATC 180
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Db 446 TCCTACCATGGCTGCTGGGTGACAAATCAGATCATGCCCCAGACAGGCTTCTCTGATAATC 505
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QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
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Db 506 GTCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 550
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RESULT 7
LOCUS BG575715 686 bp mRNA EST 10-APR-2001
DEFINITION 602598794F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4707599 5',
mRNA sequence.
ACCESSION BG575715
VERSION BG575715.1 GI:13583368
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 686)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10577 row: k column: 24
High quality sequence stop: 682.
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/lab_host="DH10B (phage-resistant)"
/note="Organ: breast; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dr primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 148 a 176 c 209 g 153 t
ORIGIN

Query Match 95.0%; Score 213.8; DB 11; Length 686;
Best Local Similarity 96.9%; Pred. No. 5.8e-46;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db 60 TATTTCTTTCTGTGATCTTCAGCAAGCTTCAGTTCCTTGCAGCTGGTCTTTGGCATC 119
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QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACTGCTGGGCCTC 120
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QY 121 TCCTACCATGGCTGCTGGGTGACAAATCAGATCATGCCCCAGACAGGCTTCTCTGATAATC 180
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Db 180 TCCTACCATGGCTGCTGGGTGACAAATCAGATCATGCCCCAGACAGGCTTCTCTGATAATC 239
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QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
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Db 240 GTCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 284
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RESULT 8
LOCUS BI090658 704 bp mRNA EST 20-JUN-2001
DEFINITION 602853894F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4995238 5',
mRNA sequence.
ACCESSION BI090658
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VERSION KEYWORDS SOURCE	BI090658.1 EST. human.	GI:14508988
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
AUTHORS	NIH-MGC <a href="http://mgi.nci.nih.gov/">http://mgi.nci.nih.gov/</a> .	
TITLE	1 (bases 1 to 704)	
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)	
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-re@mail.nih.gov">cgapbs-re@mail.nih.gov</a> Tissue Procurement: ATCC cDNA library Prepared by: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLAM11018 row: 1 column: 23 High quality sequence stop: 703.	
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BASE COUNT	158 a	174 c 214 g 157 t 1 others
ORIGIN	Query Match 95.0%; Score 213.8; DB 11; Length 704; Best Local Similarity 96.9%; Pred. No. 5.8e-46; Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	
	QY 1 TATTTCTTCTGTGATCTTCAGAAAGCTTCGATTCCTTGAGCTGGTCTTTGGGCATC 60       Db 154 TATTTCTTCTGTGATCTTCAGAAAGCTTCGATTCCTTGAGCTGGTCTTTGGGCATC 213 	
	QY 61 GAGCTGATGGAAGTGGACCCATCGGCCACTGTACATCTTTGCCACCTGCCTGGGCCTC 120       Db 214 GAGCTGATGGAAGTGGACCCATCGGCCACTGTACATCTTTGCCACCTGCCTGGGCCTC 273 	
	QY 121 TCCTACGATGGCTGTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTCGTATATC 180       Db 274 TCCTACGATGGCTGTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTCGTATATC 333 	
	QY 181 ATCTGGCCATAATCGCAAGAGGGCGACTGTGCCCTCGAGGAG 225       Db 334 GTCTGGCCATAATCGCAAGAGGGCGACTGTGCCCTCGAGGAG 378 	
RESULT 9	BG765526	
LOCUS	BG765526	769 bp mRNA EST 15-MAY-2001
DEFINITION	602739439F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4869321 5', mRNA sequence.	
ACCESSION	BG765526	
VERSION	BG765526.1 GI:14076179	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
AUTHORS	1 (bases 1 to 769)	
TITLE	NIH-MGC <a href="http://mgi.nci.nih.gov/">http://mgi.nci.nih.gov/</a> . National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-re@mail.nih.gov">cgapbs-re@mail.nih.gov</a> Tissue Procurement: ATCC cDNA library Prepared by: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLAM11018 row: 1 column: 23 High quality sequence stop: 703.	
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BASE COUNT	158 a	174 c 214 g 157 t 1 others
ORIGIN	Query Match 95.0%; Score 213.8; DB 11; Length 704; Best Local Similarity 96.9%; Pred. No. 5.8e-46; Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	
	QY 1 TATTTCTTCTGTGATCTTCAGAAAGCTTCGATTCCTTGAGCTGGTCTTTGGGCATC 60       Db 154 TATTTCTTCTGTGATCTTCAGAAAGCTTCGATTCCTTGAGCTGGTCTTTGGGCATC 213 	
	QY 61 GAGCTGATGGAAGTGGACCCATCGGCCACTGTACATCTTTGCCACCTGCCTGGGCCTC 120       Db 214 GAGCTGATGGAAGTGGACCCATCGGCCACTGTACATCTTTGCCACCTGCCTGGGCCTC 273 	
	QY 121 TCCTACGATGGCTGTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTCGTATATC 180       Db 274 TCCTACGATGGCTGTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTCGTATATC 333 	
	QY 181 ATCTGGCCATAATCGCAAGAGGGCGACTGTGCCCTCGAGGAG 225       Db 334 GTCTGGCCATAATCGCAAGAGGGCGACTGTGCCCTCGAGGAG 378 	
RESULT 9	BG765526	
LOCUS	BG765526	769 bp mRNA EST 15-MAY-2001
DEFINITION	602739439F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4869321 5', mRNA sequence.	
ACCESSION	BG765526	
VERSION	BG765526.1 GI:14076179	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
AUTHORS	1 (bases 1 to 769)	
TITLE	NIH-MGC <a href="http://mgi.nci.nih.gov/">http://mgi.nci.nih.gov/</a> . National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-re@mail.nih.gov">cgapbs-re@mail.nih.gov</a> Tissue Procurement: ATCC/DCTD/DTF	
FEATURES	Location/Qualifiers	
source	1..769 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4869321" /lab_host="NIH_MGC_49" /tissue_type="melanotic melanoma, high MDR (cell line)" /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."	
BASE COUNT	161 a	218 c 222 g 168 t
ORIGIN	Query Match 95.0%; Score 213.8; DB 11; Length 769; Best Local Similarity 96.9%; Pred. No. 5.9e-46; Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	
	QY 1 TATTTCTTCTGTGATCTTCAGAAAGCTTCGATTCCTTGAGCTGGTCTTTGGGCATC 60       Db 374 TATTTCTTCTGTGATCTTCAGAAAGCTTCGATTCCTTGAGCTGGTCTTTGGGCATC 433 	
	QY 61 GAGCTGATGGAAGTGGACCCATCGGCCACTGTACATCTTTGCCACCTGCCTGGGCCTC 120       Db 434 GAGCTGATGGAAGTGGACCCATCGGCCACTGTACATCTTTGCCACCTGCCTGGGCCTC 493 	
	QY 121 TCCTACGATGGCTGTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTCGTATATC 180       Db 494 TCCTACGATGGCTGTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTCGTATATC 553 	
	QY 181 ATCTGGCCATAATCGCAAGAGGGCGACTGTGCCCTCGAGGAG 225       Db 554 GTCTGGCCATAATCGCAAGAGGGCGACTGTGCCCTCGAGGAG 598 	
RESULT 10	BG280738	
LOCUS	BG280738	934 bp mRNA EST 21-FEB-2001
DEFINITION	602401029F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4543566 5', mRNA sequence.	
ACCESSION	BG280738	
VERSION	BG280738.1 GI:13029662	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
AUTHORS	1 (bases 1 to 934)	
TITLE	NIH-MGC <a href="http://mgi.nci.nih.gov/">http://mgi.nci.nih.gov/</a> .	
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)	
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-re@mail.nih.gov">cgapbs-re@mail.nih.gov</a> Tissue Procurement: ATCC/DCTD/DTF	

cdna Library Preparation: Ling Hong/Rubin Laboratory  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
Plate: LICM1225 row: i column: 07  
High quality sequence stop: 673.

FEATURES  
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1..934  
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/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: skin; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; cdna made by oligo-dt priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCAGGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
BASE COUNT 235 a 266 c 267 g 166 t  
ORIGIN

Query Match 90.0%; Score 202.6; DB 11; Length 934;  
Best Local Similarity 95.9%; Pred. No. 5e-43; Indels 0; Gaps 0;  
Matches 208; Conservative 0; Mismatches 9;  
Qy 1 TATTTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCATC 60  
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Db 418 TATTTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCATC 477  
Qy 61 GAGCTGATGGAAGTGGACCCATCGGCCAGCTGTACATCTTTGGCACCTGCTGGGCCTC 120  
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Db 478 GAGCTGATGGAAGTGGACCCATCGGCCAGCTGTACATCTTTGGCACCTGCTGGGCCTC 537  
Qy 121 TCCTACGATGGCTCTGGGTGACATCAGATCATGCCAGCAGGCTTCCTGATAATC 180  
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Db 538 TCCTACGATGGCTCTGGGTGACATCAGATCATGCCAGCAGGCTTCCTGATAATC 597  
Qy 181 ATCTCTGGCCATAATCGCAAGAGAGGGCGACTGTGCC 217  
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Db 598 GTCTCTGGCCATAATCGCAAGAGAGGGCGACTGTGCC 634

## RESULT 11

BE541476  
LOCUS BE541476 795 bp mRNA EST 09-AUG-2000  
DEFINITION 601067928F1 NIH\_MGC\_10 Homo sapiens cdna clone IMAGE:3454135 5',  
mRNA sequence.  
ACCESSION BE541476  
VERSION BE541476.1 GI:9770121  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 795)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC

cdna Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: Incyte Genomics, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov

Plate: L1AM8438 row: h column: 08  
High quality sequence stop: 662.

FEATURES  
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Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.5 kb. Library prepared by Life  
Technologies."  
BASE COUNT 182 a 199 c 234 g 180 t  
ORIGIN

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Best Local Similarity 96.9%; Pred. No. 1e-42; Indels 1; Gaps 1;  
Matches 216; Conservative 0; Mismatches 6;  
Qy 3 TTTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCATCGA 62  
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Db 189 TTTCTTCGTGTGATCTTCAGCAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCATCGA 247

Qy 63 GCTGATGGAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCACCTGCTGGGCCTCTC 122  
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Db 248 GCTGATGGAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCACCTGCTGGGCCTCTC 307

Qy 123 CTAGATGGCTCTGGGTGACATCAGATCATGCCAGGACAGCTTCCTGATAATCAT 182

Db 308 CTAGATGGCTCTGGGTGACATCAGATCATGCCAGGACAGCTTCCTGATAATCAT 367

Qy 183 CCTGSCATAATCGCAAGAGGGCGACTGTGCCCTGAGGAG 225  
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Db 368 CCTGSCATAATCGCAAGAGGGCGACTGTGCCCTGAGGAG 410

## RESULT 12

BE897495  
LOCUS BE897495 590 bp mRNA EST 20-OCT-2000  
DEFINITION 601432326F1 NIH\_MGC\_72 Homo sapiens cdna clone IMAGE:3917503 5',  
mRNA sequence.  
ACCESSION BE897495  
VERSION BE897495.1 GI:10363014  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 590)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP  
cdna Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov

Plate: L1AM9744 row: c column: 08  
High quality sequence stop: 589.

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Matches 207;	Conservative	0;	Mismatches 17;	Indels 0;
Gaps 0;				

[illegible]

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QY	122	CCTACGATGGCTCTCTGGGTGCACAAATCAGATCATGCCAGGACAGGCTTCCTGATAATCA	181
Db	343	CCTACGATGGCTCTCTGGGCGACAATCAGATCTGTGCCAAGACAGGCTCCTGATAATCG	402
QY	182	TCCGTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG	225
Db	403	TCCTGGCCATAATCGCAAAAGAGGGCGACTGTGCCCTGAGGAG	446

RESULT	14				
BI086876					
LOCUS	BI086876	768 bp	mRNA	EST	20-JUN-2001

ACCESSION	BI086876	miRNA sequence.
VERSION	BI086876.1	GI:14505206
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 768)  
N1H-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Incyte Genomics, Inc.  
CDNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1AM11010 row: k column: 24  
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Location/Qualifiers  
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FEATURES  
SOURCE

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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5 kb. Library prepared by Life
Technologies."
BASE COUNT      170 a      227 c      212 g      158 t      1 others
ORIGIN

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Best Local Similarity 96.8%; Pred. No. 2e-41;
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Db 658 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGAGGCTTCCTGTATAATC 717  
QY 181 ATCTTGCCAT-ATCCGACAGAGGGGAGTGTGCC 217  
Db 718 ATCTGTGCATAATCGCAAAAGAGGGCGATTGTGCC 755

RESULT 15  
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DEFINITION mRNA sequence.  
ACCESSION BI092532  
VERSION BI092532.1 GI:14510862  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 767)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Incyte Genomics, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM1026 row: b column: 23  
High quality sequence stop: 643.  
Location/Qualifiers  
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/cell\_line="MGC36"  
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Site2: SalI; Cloned unidirectionally. Primer: Oligo dr.  
Average insert size 1.5 kb. Library prepared by Life  
Technologies."

BASE COUNT 164 a 227 c 224 g 152 t  
ORIGIN

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Best Local Similarity 95.1%; Pred. No. 2.6e-41;  
Matches 213; Conservative 0; Mismatches 10; Indels 1; Gaps 1;  
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QY 61 GAGCTGATGAAGTGAGCCCATCGGCCAGCTGACATCTTTGCCACCTGCTGGGGCTC 120  
Db 494 GAGCTGATGAAGTGAGCCCATCGGCCAGCTTGTACATCTTTGCCACCTGCTGGGGCTC 553  
QY 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGAGGCTTCCTGTATAATC 180

Db 554 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGAGGCTTCCTGTATAATC 613  
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
1352.018 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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4	225	100.0	225	3	US-08-967-727-18
5	225	100.0	225	4	US-08-037-230D-18
6	220.2	97.9	945	4	US-09-056-105-7
7	220.2	97.9	1019	4	US-09-056-103-13
8	220.2	97.9	1375	2	US-08-993-738A-2
9	220.2	97.9	1375	4	US-08-713-354C-2
10	213.8	95.0	1640	1	US-07-807-043B-11
11	213.8	95.0	1640	1	US-08-299-849B-11
12	213.8	95.0	1640	2	US-08-142-368A-11
13	213.8	95.0	1640	3	US-08-967-727-11
14	213.8	95.0	1640	4	US-08-037-230D-11
15	213.8	95.0	4204	2	US-08-928-615-1
16	213.8	95.0	4204	4	US-09-056-105-6
17	213.8	95.0	4204	4	US-09-166-448-1
18	195.2	86.8	4157	1	US-07-807-043B-9
19	195.2	86.8	4157	1	US-08-299-849B-9
20	195.2	86.8	4157	2	US-08-142-368A-9
21	195.2	86.8	4157	3	US-08-967-727-9
22	195.2	86.8	4157	4	US-08-037-230D-9
23	195.2	86.8	4559	4	US-09-056-105-5
24	163.2	72.5	1084	2	US-08-184-009-110
25	163.2	72.5	1084	2	US-08-458-356-110
26	163.2	72.5	1084	4	US-08-460-736-110
27	163.2	72.5	1094	2	US-08-184-009-109

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29	163.2	72.5	1094	4	US-08-460-736-109	Sequence 109, App
30	163.2	72.5	1691	2	US-08-993-118-8	Sequence 8, Appli
31	163.2	72.5	1691	3	US-08-845-528C-8	Sequence 8, Appli
32	163.2	72.5	2419	1	US-07-807-043B-7	Sequence 7, Appli
33	163.2	72.5	2419	1	US-08-299-849B-7	Sequence 7, Appli
34	163.2	72.5	2419	2	US-08-142-368A-7	Sequence 7, Appli
35	163.2	72.5	2419	3	US-08-967-727-7	Sequence 7, Appli
36	163.2	72.5	2419	4	US-08-037-230D-7	Sequence 7, Appli
37	163.2	72.5	2420	1	US-08-465-167A-23	Sequence 23, Appli
38	163.2	72.5	2420	4	US-09-056-105-4	Sequence 4, Appli
39	163.2	72.5	5674	1	US-07-807-043B-8	Sequence 8, Appli
40	163.2	72.5	5674	1	US-08-190-411A-1	Sequence 1, Appli
41	163.2	72.5	5674	1	US-08-299-849B-8	Sequence 8, Appli
42	163.2	72.5	5674	2	US-08-560-024-1	Sequence 1, Appli
43	163.2	72.5	5674	2	US-08-142-368A-8	Sequence 8, Appli
44	163.2	72.5	5674	3	US-08-967-727-8	Sequence 8, Appli
45	163.2	72.5	5674	4	US-08-037-230D-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1  
US-07-807-043B-15  
; Sequence 15, Application US/07807043B  
; Patent No..5342774  
; GENERAL INFORMATION:  
; APPLICANT: Boon, Thierry, Van den Eynde, Beno t  
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor  
; TITLE OF INVENTION: Rejection Antigens and Uses Thereof  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York City  
; STATE: New York  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
; COMPUTER: IBM  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/807,043B  
; FILING DATE: 19911212  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/764,364  
; FILING DATE: 23-SEPTEMBER-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/728,838  
; FILING DATE: 9-JULY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/705,702  
; FILING DATE: 23-May-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hansop, No. 5342774man D.  
; REGISTRATION NUMBER: 30,946  
; REFERENCE/DOCKET NUMBER: LUD 253.3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 225 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: singular  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: MAGE-6 gene  
US-07-807-043B-15

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Query Match      100.0%; Score 225; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 4e-62;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCCGATTCTTGCAGCTGGTCTTTGGCATC 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCCGATTCTTGCAGCTGGTCTTTGGCATC 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGGCACCTGCTGGGCTC 120
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGGCACCTGCTGGGCTC 120
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGACAGGCTTCTCTGATAATC 180
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGACAGGCTTCTCTGATAATC 180
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 181 ATCCTGGCCATAATCGCAAGAGAGGGGACTGTGCCCTGAGGAG 225
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 ATCCTGGCCATAATCGCAAGAGAGGGGACTGTGCCCTGAGGAG 225
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RESULT 2
US-08-299-849B-18
; Sequence 18, Application us/08299849B
; Patent No. 5612201
; GENERAL INFORMATION:
; APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
; APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
; APPLICANT: Chomez, Patrick
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
; TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/299,849B
; FILING DATE: 1-SEPTEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5612201man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5355
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200

; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: MAGE-6 gene
US-08-299-849B-18

Query Match      100.0%; Score 225; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 4e-62;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCCGATTCTTGCAGCTGGTCTTTGGCATC 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCCGATTCTTGCAGCTGGTCTTTGGCATC 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGGCACCTGCTGGGCTC 120
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGGCACCTGCTGGGCTC 120
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGACAGGCTTCTCTGATAATC 180
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGACAGGCTTCTCTGATAATC 180
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 181 ATCCTGGCCATAATCGCAAGAGAGGGGACTGTGCCCTGAGGAG 225
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 ATCCTGGCCATAATCGCAAGAGAGGGGACTGTGCCCTGAGGAG 225
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3
US-08-142-368A-18
; Sequence 18, Application US/08142368A
; Patent No. 5925729
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;
; APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
; APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
; TITLE OF INVENTION: Rejection Antigens and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,368A
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
```



APPLICATION NUMBER: 07/705,702  
FILING DATE: 23-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5925729man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5253.4-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 225 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: MAGE-6 gene  
US-08-142-368A-18

Query Match 100.0%; Score 225; DB 2; Length 225;  
Best Local Similarity 100.0%; Pred. No. 4e-62;  
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TATTTCTTCCGTGATCTTCAGCAAGCTTCGGATTCCCTTCAGCTGCTTTTGGCATC 60  
Db 1 TATTTCTTCCGTGATCTTCAGCAAGCTTCGGATTCCCTTCAGCTGCTTTTGGCATC 60  
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCGTGGCCCTC 120  
Db 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCGTGGCCCTC 120  
QY 121 TCCTAGATGGCTGCTGGGTGACATCATCGCCACGTGTACATCTTTGCCACCTGCGTGGCCCTC 180  
Db 121 TCCTAGATGGCTGCTGGGTGACATCATCGCCACGTGTACATCTTTGCCACCTGCGTGGCCCTC 180  
QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGGACTGTGCCCTTGAGGAG 225  
Db 181 ATCTGGCCATAATCGCAAGAGAGGGCGGACTGTGCCCTTGAGGAG 225

RESULT 4  
US-08-967-727-18  
Sequence 18, Application US/08967727  
Patent No. 6025474  
GENERAL INFORMATION:  
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;  
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry  
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For  
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/967,727  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037,230  
FILING DATE: 26-MARCH-1993  
APPLICATION NUMBER: PCT/US92/04354  
FILING DATE: 22-MAY-1992  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: 07/807,043  
FILING DATE: 12-DECEMBER-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/764,365  
FILING DATE: 23-SEPTEMBER-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/728,838  
FILING DATE: 9-JULY-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/705,702  
FILING DATE: 23-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 6025474man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5353  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 225 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: MAGE-6 gene  
US-08-967-727-18  
Query Match 100.0%; Score 225; DB 3; Length 225;  
Best Local Similarity 100.0%; Pred. No. 4e-62;  
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TATTTCTTCCGTGATCTTCAGCAAGCTTCGGATTCCCTTCAGCTGCTTTTGGCATC 60  
Db 1 TATTTCTTCCGTGATCTTCAGCAAGCTTCGGATTCCCTTCAGCTGCTTTTGGCATC 60  
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCGTGGCCCTC 120  
Db 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCGTGGCCCTC 120  
QY 121 TCCTAGATGGCTGCTGGGTGACATCATCGCCACGTGTACATCTTTGCCACCTGCGTGGCCCTC 180  
Db 121 TCCTAGATGGCTGCTGGGTGACATCATCGCCACGTGTACATCTTTGCCACCTGCGTGGCCCTC 180  
QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGGACTGTGCCCTTGAGGAG 225  
Db 181 ATCTGGCCATAATCGCAAGAGAGGGCGGACTGTGCCCTTGAGGAG 225  
RESULT 5  
US-08-037-230D-18  
Sequence 18, Application US/08037230D  
Patent No. 6235525  
GENERAL INFORMATION:  
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;  
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry  
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For  
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/037, 230D  
;; FILING DATE: 26-MARCH-1993  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US92/04354  
;; FILING DATE: 22-MAY-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/807,043  
;; FILING DATE: 12-DECEMBER-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/764,364  
;; FILING DATE: 23-SEPTEMBER-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/728,838  
;; FILING DATE: 9-JULY-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/705,702  
;; FILING DATE: 23-MAY-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Hanson, No. 6235525man D.  
;; REGISTRATION NUMBER: 30,946  
;; REFERENCE/DOCKET NUMBER: LUD 5353  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 688-9200  
;; TELEFAX: (212) 838-3884  
;; INFORMATION FOR SEQ ID NO: 18:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 225 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA  
;; FEATURE:  
;; NAME/KEY: MAGE-6 gene  
US-08-037-230D-18

Query Match 100.0%; Score 225; DB 4; Length 225;  
Best Local Similarity 100.0%; Pred. No. 4e-62;  
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TATTTCTTTCTGTGATCTTCAGCAAAAGCTTCGCAATCTTCCTTGCAGCTGGTCTTTGGCATC 60  
Db 1 TATTTCTTTCTGTGATCTTCAGCAAAAGCTTCGCAATCTTCCTTGCAGCTGGTCTTTGGCATC 60  
Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGGCACCTGCTGGGCCTC 120  
Db 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGGCACCTGCTGGGCCTC 120  
Qy 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGTGCCCAGACAGGCTTCCTGATAATC 180  
Db 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGTGCCCAGACAGGCTTCCTGATAATC 180  
Qy 181 ATCTGGCCATAATCGCAAGAGAGGGCGACGTGCTGCCCTGAGGAG 225  
Db 181 ATCTGGCCATAATCGCAAGAGAGGGCGACGTGCTGCCCTGAGGAG 225

RESULT 6  
US-09-056-105-7  
; Sequence 7, Application US/09056105  
; Patent No. 6287569  
; GENERAL INFORMATION:  
; APPLICANT: KIPPS, THOMAS J.  
; APPLICANT: WU, YUNQI  
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR  
; FILE REFERENCE: 233/221  
; CURRENT APPLICATION NUMBER: US/09/056,105  
; EARLIER FILING DATE: 1998-04-06  
; EARLIER APPLICATION NUMBER: 60/043,467  
; NUMBER OF SEQ ID NOS: 35

;; SOFTWARE: FastSEQ for Windows Version 3.0  
;; SEQ ID NO 7  
;; LENGTH: 945  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-056-105-7

Query Match 97.9%; Score 220.2; DB 4; Length 945;  
Best Local Similarity 98.7%; Pred. No. 2.4e-60;  
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 TATTTCTTTCTGTGATCTTCAGCAAAAGCTTCGCAATCTTCCTTGCAGCTGGTCTTTGGCATC 60  
Db 433 tactttctctgtgattcttcagcaaaagcttcagattcttcagctggtcttttgccatc 492  
Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGGCACCTGCTGGGCCTC 120  
Db 493 gagctgatggaagtggaccacctcgccacgtgtacatctttgcccacctgctgggacctc 552  
Qy 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGTGCCCAGACAGGCTTCCTGATAATC 180  
Db 553 tctacgatggcctgctgggtgacaatcagatcatgcccagacaggtctctctgataatc 612  
Qy 181 ATCTGGCCATAATCGCAAGAGAGGGCGACGTGCTGCCCTGAGGAG 225  
Db 613 atcctggccataatcgcaaaagaggcgactgtgccctgaggag 657

RESULT 7  
US-09-056-105-13  
; Sequence 13, Application US/09056105  
; Patent No. 6287569  
; GENERAL INFORMATION:  
; APPLICANT: KIPPS, THOMAS J.  
; APPLICANT: WU, YUNQI  
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR  
; FILE REFERENCE: 233/221  
; CURRENT APPLICATION NUMBER: US/09/056,105  
; CURRENT FILING DATE: 1998-04-06  
; EARLIER APPLICATION NUMBER: 60/043,467  
; EARLIER FILING DATE: 1997-04-10  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 1019  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-056-105-13

Query Match 97.9%; Score 220.2; DB 4; Length 1019;  
Best Local Similarity 98.7%; Pred. No. 2.5e-60;  
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 TATTTCTTTCTGTGATCTTCAGCAAAAGCTTCGCAATCTTCCTTGCAGCTGGTCTTTGGCATC 60  
Db 498 tactttctctgtgattcttcagcaaaagcttcagattcttcagctggtcttttgccatc 557  
Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGGCACCTGCTGGGCCTC 120  
Db 558 gagctgatggaagtggaccacctcgccacgtgtacatctttgcccacctgctgggacctc 617  
Qy 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGTGCCCAGACAGGCTTCCTGATAATC 180  
Db 618 tctacgatggcctgctgggtgacaatcagatcatgcccagacaggtctctctgataatc 677  
Qy 181 ATCTGGCCATAATCGCAAGAGAGGGCGACGTGCTGCCCTGAGGAG 225  
Db 678 atcctggccataatcgcaaaagaggcgactgtgccctgaggag 722

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RESULT 8
US-08-993-738A-2
; Sequence 2, Application US/08993738A
; Patent No. 5928938
; GENERAL INFORMATION:
; APPLICANT: van der Bruggen, Pierre; DePaeen Etienne;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Complex With
; TITLE OF INVENTION: HLA-Cw*16 Molecules, and Uses Thereof
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,738A
; FILING DATE: 19-December-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,354
; FILING DATE: 13-September-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5928938man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5460.1 DIV - JEL/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1375 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-993-738A-2

Query Match 97.9%; Score 220.2; DB 2; Length 1375;
Best Local Similarity 98.7%; Pred. No. 2.8e-60;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTCTTTCTCTGATCTTCAGCAAGCTTCGAGTTCCCTTGCGAGCTGGTCTTTGGCATC 60
|| |||||
Db 592 TACTTCTTTCTCTGATCTTCAGCAAGCTTCGAGTTCCCTTGCGAGCTGGTCTTTGGCATC 651
|| |||||

QY 61 GAGCTGATGGAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCACCTGCCTGGGCGCTC 120
|| |||||
Db 652 GAGCTGATGGAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCACCTGCCTGGGCGCTC 711
|| |||||

QY 121 TCCTAGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180
|| |||||
Db 712 TCCTAGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGGCTTCCTGATAATC 771
|| |||||

QY 181 ATCTGGCCATAATCCAGAGAGGGCGACTGTGCCCTGAGGAG 225
|| |||||
Db 772 ATCTGGCCATAATCCAGAGAGGGCGACTGTGCCCTGAGGAG 816
|| |||||

RESULT 9
US-08-713-354C-2
; Sequence 2, Application US/08713354C
; Patent No. 6285215
; GENERAL INFORMATION:
; APPLICANT: van der Bruggen, Pierre; DePaeen Etienne;
```

```
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Complex With
; TITLE OF INVENTION: HLA-Cw*16 Molecules, and Uses Thereof
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,354C
; FILING DATE: 13-September-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6265215man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5460
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1375 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-713-354C-2

Query Match 97.9%; Score 220.2; DB 4; Length 1375;
Best Local Similarity 98.7%; Pred. No. 2.8e-60;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTCTTTCTCTGATCTTCAGCAAGCTTCGAGTTCCCTTGCGAGCTGGTCTTTGGCATC 60
|| |||||
Db 592 TACTTCTTTCTCTGATCTTCAGCAAGCTTCGAGTTCCCTTGCGAGCTGGTCTTTGGCATC 651
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QY 61 GAGCTGATGGAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCACCTGCCTGGGCGCTC 120
|| |||||
Db 652 GAGCTGATGGAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCACCTGCCTGGGCGCTC 711
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QY 121 TCCTAGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180
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Db 712 TCCTAGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGGCTTCCTGATAATC 771
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QY 181 ATCTGGCCATAATCCAGAGAGGGCGACTGTGCCCTGAGGAG 225
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Db 772 ATCTGGCCATAATCCAGAGAGGGCGACTGTGCCCTGAGGAG 816
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RESULT 10
US-07-807-043B-11
; Sequence 11, Application US/07807043B
; Patent No. 5342774
; GENERAL INFORMATION:
; APPLICANT: Boon, Thierry, Van den Eynde, Beno t
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
; TITLE OF INVENTION: Rejection Antigens and Uses Thereof
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
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COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/807,043B  
FILING DATE: 19911212  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/764,364  
FILING DATE: 23-SEPTEMBER-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/728,838  
FILING DATE: 9-JULY-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/705,702  
FILING DATE: 23-May-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5342774man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 253.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1640 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: singular  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: cDNA MAGE-3  
US-07-807-043B-11

Query Match 95.0%; Score 213.8; DB 1; Length 1640;  
Best Local Similarity 96.9%; Pred. No. 3.1e-56;  
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
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Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGGCACCTGCCTGGGCCTC 120  
Db 664 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGGCACCTGCCTGGGCCTC 723  
Qy 121 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCAGACAGGCTTCCTGATAATC 180  
Db 724 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCAGACAGGCTTCCTGATAATC 783  
Qy 181 ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225  
Db 784 GTCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 828

RESULT 11  
US-08-299-849B-11  
Sequence 11, Application US/08299849B  
Patent No. 5612201  
GENERAL INFORMATION:  
APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;  
APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;  
APPLICANT: Chomez, Patrick  
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In  
TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/299,849B  
FILING DATE: 1-SEPTEMBER-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037,230  
FILING DATE: 26-MARCH-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/04354  
FILING DATE: 22-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/807,043  
FILING DATE: 12-DECEMBER-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/764,364  
FILING DATE: 23-SEPTEMBER-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/728,838  
FILING DATE: 9-JULY-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/705,702  
FILING DATE: 23-May-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5612201man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5355  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1640 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: cDNA MAGE-3  
US-08-299-849B-11

Query Match 95.0%; Score 213.8; DB 1; Length 1640;  
Best Local Similarity 96.9%; Pred. No. 3.1e-58;  
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATC 60  
Db 604 TATTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATC 663  
Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGGCACCTGCCTGGGCCTC 120  
Db 664 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGGCACCTGCCTGGGCCTC 723  
Qy 121 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCAGACAGGCTTCCTGATAATC 180  
Db 724 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCAGACAGGCTTCCTGATAATC 783  
Qy 181 ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225  
Db 784 GTCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 828  
RESULT 12  
US-08-142-368A-11  
Sequence 11, Application US/08142368A  
Patent No. 5925729  
GENERAL INFORMATION:  
APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;

APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;  
APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia  
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor  
TITLE OF INVENTION: Rejection Antigens and Uses Thereof  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022

COMPUTER READABLE FORM: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/142,368A  
FILING DATE: 02-MAY-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/04354  
FILING DATE: 22-MAY-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/807,043  
FILING DATE: 12-DECEMBER-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/764,364  
FILING DATE: 23-SEPTEMBER-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/728,838  
FILING DATE: 9-JULY-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/705,702  
FILING DATE: 23-MAY-1991

ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5925729man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5253.4-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1640 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: CDNA MAGE-3

US-08-142-368A-11

Query Match 95.0%; Score 213.8; DB 2; Length 1640;  
Best Local Similarity 96.9%; Pred. No. 3.1e-58;  
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCGAGTTCCTTGAGCTGGTCTTTGGCATC 60  
Db 604 TATTTCTTCTGTGATCTTCAGCAAGCTTCGAGTTCCTTGAGCTGGTCTTTGGCATC 663

QY 61 GAGCTGATGGAAGTGGACCCCATCGGCGAGTGTACATCTTTGCCACCTGCGTGGCCCTC 120  
Db 664 GAGCTGATGGAAGTGGACCCCATCGGCGAGTGTACATCTTTGCCACCTGCGTGGCCCTC 723

QY 121 TCCTACGATGGCTGCTGGTGGTGAACATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180  
Db 724 TCCTACGATGGCTGCTGGTGGTGAACATCAGATCATGCCAGGACAGGCTTCCTGATAATC 783

QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTTGAGGAG 225  
Db 784 GTCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTTGAGGAG 828

RESULT 13

US-08-967-727-11  
; Sequence 11, Application US/08967727  
; Patent No. 6025474

GENERAL INFORMATION:  
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;  
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry  
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For  
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022

COMPUTER READABLE FORM: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/967,727  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037,230  
FILING DATE: 26-MARCH-1993  
APPLICATION NUMBER: PCT/US92/04354  
FILING DATE: 22-MAY-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/807,043  
FILING DATE: 12-DECEMBER-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/764,365  
FILING DATE: 23-SEPTEMBER-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/728,838  
FILING DATE: 9-JULY-1991

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/705,702  
FILING DATE: 23-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 6025474man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5353  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1640 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: CDNA MAGE-3

US-08-967-727-11

Query Match 95.0%; Score 213.8; DB 3; Length 1640;  
Best Local Similarity 96.9%; Pred. No. 3.1e-58;  
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCGAGTTCCTTGAGCTGGTCTTTGGCATC 60  
Db 604 TATTTCTTCTGTGATCTTCAGCAAGCTTCGAGTTCCTTGAGCTGGTCTTTGGCATC 663

QY 61 GAGCTGATGGAAGTGGACCCCATCGGCGAGTGTACATCTTTGCCACCTGCGTGGCCCTC 120  
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Db 664 GAGCTGATGGAAGTGGACCCCATGGCCACTGTGTACATCTTTGGCCACCTGCTGGGCCTC 723  
QY 121 TCCTACGATGCGCTCTGGGTGACAAATCAGATCATGCCAGACAGGCTTCTGTGATAATC 180  
Db 724 TCCTACGATGCGCTCTGGGTGACAAATCAGATCATGCCAAGGAGGCGCTCTGTGATAATC 783  
QY 181 ATCTGCGCCATAATCGCAAGAGAGGGCGACTGTGCCCCCTGAGGAG 225  
Db 784 GTCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCCCTGAGGAG 828  
RESULT 14  
US-08-037-230D-11  
; Sequence 11, Application US/08037230D  
; Patent No. 6235525  
; GENERAL INFORMATION:  
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;  
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry  
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For  
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York City  
; STATE: New York  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
; COMPUTER: IBM  
; OPERATING SYSTEM: PC-DOS  
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; APPLICATION NUMBER: US/08/037,230D  
; FILING DATE: 26-MARCH-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/04354  
; FILING DATE: 22-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/807,043  
; FILING DATE: 12-DECEMBER-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/764,364  
; FILING DATE: 23-SEPTEMBER-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/728,838  
; FILING DATE: 9-JULY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/705,702  
; FILING DATE: 23-MAY-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hanson, No. 6235525man D.  
; REGISTRATION NUMBER: 30,946  
; REFERENCE/DOCKET NUMBER: LUD 5353  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1640 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA to mRNA  
; FEATURE:  
; NAME/KEY: CDNA MAGE-3  
US-08-037-230D-11  
Query Match 95.0%; Score 213.8; DB 4; Length 1640;  
Best Local Similarity 96.9%; Pred. No. 3.le-58;  
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTTCCTTCTGTGATCTTCAGCAAGCTTCCGATTCTCTTCAGCTGGTCTTTGGCATC 60  
Db 604 TATTTCCTTCTGTGATCTTCAGCAAGCTTCCGATTCTCTTCAGCTGGTCTTTGGCATC 663  
QY 61 GAGCTGATGGAAGTGGAGCCCATCGGCCACGTGTACATCTTTTGGCCACCTGCTGGGCCTC 120  
Db 664 GAGCTGATGGAAGTGGAGCCCATCGGCCACGTGTACATCTTTTGGCCACCTGCTGGGCCTC 723  
QY 121 TCCTACGATGCGCTCTGGGTGACAAATCAGATCATGCCAGACAGGCTTCTGTGATAATC 180  
Db 724 TCCTACGATGCGCTCTGGGTGACAAATCAGATCATGCCAAGGAGGCGCTCTGTGATAATC 783  
QY 181 ATCTGCGCCATAATCGCAAGAGAGGGCGACTGTGCCCCCTGAGGAG 225  
Db 784 GTCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCCCTGAGGAG 828  
RESULT 15  
US-08-928-615-1  
; Sequence 1, Application US/08928615  
; Patent No. 5965535  
; GENERAL INFORMATION:  
; APPLICANT: Chau, Pascal  
; APPLICANT: Stroobant, Vincent  
; APPLICANT: Boon, Thierry  
; APPLICANT: van der Bruggen, Pierre  
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED  
; TITLE OF INVENTION: BY HLA CLASS II MOLECULES  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: MA  
; COUNTRY: U.S.A.  
; ZIP: 02210-2211  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/928,615  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Van Amsterdam, John R.  
; REGISTRATION NUMBER: 40,212  
; REFERENCE/DOCKET NUMBER: L0461/7017  
; TELEPHONE: 617-720-3500  
; TELEFAX: 617-720-2441  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4204 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 2465...3406  
US-08-928-615-1  
Query Match 95.0%; Score 213.8; DB 2; Length 4204;  
Best Local Similarity 96.9%; Pred. No. 4.6e-58;  
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTTCCTTCTGTGATCTTCAGCAAGCTTCCGATTCTCTTCAGCTGGTCTTTGGCATC 60

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QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGCTGTACATCTTTGGCCACCTGSCCTGGGCCTC 120
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Db 2957 GAGCTGATGGAAGTGGACCCCATCGGCCACTTGTACATCTTTGCCACCTGGCCTGGGCCTC 3016
QY 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCCAGGAGGCTTTCCTGATAATC 180
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Db 3017 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAAGGACGGCCTTCCTGATAATC 3076
QY 181 ATCCTGGCCATAATCGCAAGAGAGGGGACTGTGCCCTGAGGAG 225
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
1950.042 Million cell updates/sec

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Perfect score: 225  
Sequence: 1 TATTCTTTCCTGATCTT.....GCGACTGTGCCCTGAGGAG 225

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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22: /SIDS2/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	225	100.0	225	13 AAQ32362	MAGE-6 gene. Homo
2	225	100.0	225	15 AAQ72487	Tumour rejection a
3	225	100.0	225	20 AAX84122	MAGE-6 gene. Homo
4	223.4	99.3	225	16 AAT01166	MAGE-6 gene. Homo
5	220.2	97.9	1362	20 AAX87596	CLYTA-MAGE-3-His f
6	220.2	97.9	1375	19 AAV22716	MAGE-6 cDNA. Homo
7	220.2	97.9	4204	22 AAS02056	DNA encoding molec
8	213.8	95.0	945	22 AAD12993	Human MAGE-A3 DNA.
9	213.8	95.0	1212	20 AAX87592	Haemagglutinin-MAG
10	213.8	95.0	1353	20 AAX87588	Lipoprotein D-MAGE
11	213.8	95.0	1640	15 AAQ72480	Tumour rejection a

12	213.8	95.0	1640	20 AAX84116	MAGE-3 gene. Homo
13	213.8	95.0	4204	20 AAX26974	cDNA encoding MAGE
14	213.8	95.0	4204	21 AAA37927	Human MAGE-A3 nucl
15	212.2	94.3	1640	13 AAQ32355	MAGE-3 cDNA. Homo
16	195.2	86.8	920	22 AAI24300	Probe #14233 for g
17	195.2	86.8	920	22 AAI49576	Probe #18262 used
18	195.2	86.8	920	22 AAI15118	Probe #5051 for ge
19	195.2	86.8	1956	22 AAI36453	Probe #5139 used t
20	195.2	86.8	4157	13 AAQ32353	MAGE-2 gene. Homo
21	195.2	86.8	4157	15 AAQ72478	Tumour rejection a
22	195.2	86.8	4157	20 AAX84114	MAGE-2 gene. Homo
23	195.2	86.8	4523	22 AAD06131	Human MAGE-12 gene
24	166	73.8	379	18 AAT63345	Human MAGE-3 DNA.
25	163.2	72.5	930	22 AAD12987	Human MAGE-A1 cDNA
26	163.2	72.5	1084	15 AAQ67866	H6/MAGE-1 expressi
27	163.2	72.5	1084	20 AAZ08442	H6/MAGE-1 expressi
28	163.2	72.5	1094	15 AAQ67865	H6/MAGE-1 expressi
29	163.2	72.5	1094	20 AAZ08441	H6/MAGE-1 expressi
30	163.2	72.5	1338	20 AAX87593	CLYTA-MAGE-1-His f
31	163.2	72.5	1341	20 AAX87591	Lipoprotein D-MAGE
32	163.2	72.5	1624	22 AAF24676	Nucleotide sequenc
33	163.2	72.5	1691	20 AAF69719	Tumour rejection a
34	163.2	72.5	2418	20 AAX84103	E antigen precursor
35	163.2	72.5	2419	13 AAQ32351	Antigen E gene. H
36	163.2	72.5	2419	15 AAQ72476	Tumour rejection a
37	163.2	72.5	2419	16 AAT05086	MZ2-MEL antigen E
38	163.2	72.5	2419	20 AAX84112	Antigen E coding s
39	163.2	72.5	2420	15 AAQ72472	Tumour rejection a
40	163.2	72.5	2420	16 AAX85435	Human melanoma ant
41	163.2	72.5	5674	13 AAQ32352	MAGE-1 nucleic aci
42	163.2	72.5	5674	15 AAQ72477	Tumour rejection a
43	163.2	72.5	5674	20 AAX84113	MAGE-1 gene. Homo
44	163.2	72.5	5724	16 AAQ98902	Tumour rejection a
45	159.6	70.9	1022	20 AAX40199	MAGE-4 encoding ge

## ALIGNMENTS

RESULT	1
AAQ32362	AAQ32362 standard; DNA; 225 BP.
ID	AAQ32362
XX	AAQ32362;
AC	AAQ32362;
XX	22-APR-1993 (first entry)
DT	22-APR-1993 (first entry)
XX	MAGE-6 gene..
DE	MAGE-6 gene..
XX	Melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen;
KW	tumor rejection antigen precursor; MAGE; antigen E; gene family; ss.
XX	Homo sapiens.
OS	Homo sapiens.
XX	WO9220356-A.
PN	26-NOV-1992.
XX	26-NOV-1992.
XX	22-MAY-1992; 92WO-US04354.
XX	23-MAY-1991; 91US-0705702.
PR	09-JUL-1991; 91US-0728838.
PR	23-SEP-1991; 91US-0764364.
PR	12-DEC-1991; 91US-0807043.
XX	(LUDW-) LUDWIG INST CANCER RES.
XX	Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
PI	Van Den Eynde B, Van Der Bruggen P, Van Pel A;
XX	WPI; 1992-415460/50.
DR	Nucleic acid mol. encoding a human tumour rejection antigen
XX	
PT	

PT precursor - useful as an immunostimulant in a vaccine for  
 PT treating and preventing cancers, also useful in diagnosis  
 XX  
 XX Disclosure; Page 88; 142pp; English.

XX The sequences given in AAQ32352-69 represent a new family of genes  
 CC referred to as melanoma antigens (MAGE). The cDNAs of this gene  
 CC family were identified during the isolation of the antigen E gene.  
 CC The MAGE cDNAs, when tested, did not transfer expression of antigen  
 CC E, but they did show substantial homology to the antigen E cDNA  
 CC sequence. The MAGE DNAs share a certain degree of homology with each  
 CC other and are expressed in tumour cells including several types of  
 CC human tumor cells as well as in human tumors. MAGE expression is not  
 CC restricted to melanomas. MAGE refers to a family of tumor rejection  
 CC antigen precursors. The antigens resulting from these genes are  
 CC referred to as MAGE TRANS or melanoma antigen tumor rejection antigens.  
 CC See also AAQ32351.

XX Sequence 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;

Query Match 100.0%; Score 225; DB 13; Length 225;  
 Best Local Similarity 100.0%; Pred. NO. 3.3e-56;  
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTCCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCAGCTGGTCTTTGGCATC 60  
 DB 1 tattttctctgtgatcttcagcaaaagcttcgattcccttcgagctggtcttggcattc 60  
 QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTTGGCCACTGCTGGGCTC 120  
 DB 61 gagctgatggaagtggaccctcatcgccacgtgtacatctttggccacctgctgggctc 120  
 QY 121 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCAGGACAGCTTCCTGATATC 180  
 DB 121 tcctacgatggcctgctgggtgacaatcagatcatgccaggacagcttccctgataatc 180  
 QY 181 ATCTGCGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225  
 DB 181 atcttgccataatcgcaagagagggcgactgtgccctgaggag 225

RESULT 2

AAQ72487  
 ID AAQ72487 standard; cDNA to mRNA; 225 BP.

XX AC AAQ72487;

XX 22-JUN-1995 (first entry)

XX Tumour rejection antigen MAGE-6 cDNA.

XX Tumour rejection antigen; melanoma antigen-6; MAGE-6; MAGE-3;  
 KW cancer; cytolytic T cells; antigen D; human leucocyte antigen;  
 KW ss.

XX Homo sapiens.

XX WO9423031-A.

XX 13-OCT-1994.

XX 17-MAR-1994; 94WO-US02877.

XX 26-MAR-1993; 93US-0037230.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Boon-falleur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;

XX WPI; 1994-333192/41.

XX New tumour rejection antigen precursor MAGE3 - useful in

PT treatment and diagnosis of cancer  
 XX Example 32; Page 73; 105pp; English.

XX AAQ72487 is the cDNA sequence which codes for melanoma antigen-6  
 CC (MAGE-6). Another melanoma antigen MAGE-3 is encoded by  
 CC AAQ72470, this is a tumour rejection antigen precursor. Melanomas  
 CC characterised by the expression of MAGE-3 can be detected, or  
 CC monitored, by contacting a test sample with an agent that can  
 CC recognise MAGE-3. The melanoma can be treated by the administration  
 CC of cytolytic T cells specific for the complex of antigen D (the  
 CC mature rejection antigen derived from MAGE-3) and a human leucocyte  
 CC antigen (esp. HLA-A1).

XX Sequence 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;

Query Match 100.0%; Score 225; DB 15; Length 225;  
 Best Local Similarity 100.0%; Pred. NO. 3.3e-56;  
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTCCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCAGCTGGTCTTTGGCATC 60  
 DB 1 tattttctctgtgatcttcagcaaaagcttcgattcccttcgagctggtcttggcattc 60  
 QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCGCCACTGCTGGGCTC 120  
 DB 61 gagctgatggaagtggaccctcatcgccacgtgtacatctttggccacctgctgggctc 120  
 QY 121 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCAGGACAGCTTCCTGATATC 180  
 DB 121 tcctacgatggcctgctgggtgacaatcagatcatgccaggacaggttccctgataatc 180  
 QY 181 ATCTGCGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225  
 DB 181 atcttgccataatcgcaagagagggcgactgtgccctgaggag 225

RESULT 3

AAQ84122  
 ID AAX84122 standard; cDNA; 225 BP.

XX AC AAX84122;

XX 08-SEP-1999 (first entry)

XX MAGE-6 gene.

XX Tumour rejection antigen; vaccine; cancer; MAGE-6 gene; ss.

XX Homo sapiens.

XX US5925729-A.

XX 20-JUL-1999.

XX 02-MAY-1994; 94US-0142368.

XX 02-MAY-1994; 94US-0142368.

XX 23-MAY-1991; 91US-0705702.

XX 09-JUL-1991; 91US-0728838.

XX 23-SEP-1991; 91US-0764365.

XX 12-DEC-1991; 91US-0807043.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;

XX Van Den Eynde B, Van Der Bruggen P, Van Pel A;

XX WPI; 1999-418294/35.

XX New tumour rejection antigen is useful as a vaccine against  
 PT cancerous diseases

XX PS. Disclosure; Column 69-70; 58pp; English.  
XX  
XX This sequence represents the MAGE-6 gene sequence.  
CC The invention relates to a tumour rejection antigen sequence that is  
CC useful as a tumour rejection antigen for vaccination against cancerous  
CC conditions.  
XX  
XX Sequence 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;  
SQ

Query Match 100.0%; Score 225; DB 20; Length 225;  
Best Local Similarity 100.0%; Pred. No. 3.3e-56;  
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTCTTTCCCTGATCTTCAGCAAGCTTCGGATTCTTCAGCTGCTTTTGGCATT 60  
DB 1 tattttcttcttgatcttcagcaagcttcgattcttcagctgcttttggcattc 60  
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCCTGGCCCTC 120  
DB 61 gagctgatggaagtggaccccatcgccacgtgtacatcttttgccacctgacctggccctc 120  
QY 121 TCCTACGATGGCTGCTGGTGACATTCAGATCATGCCAGGACAGGCTTCCTGTATAATC 180  
DB 121 tctacgatggcctgctggtgacatcagatcatgccagagacaggttctctgataatc 180  
QY 181 ATCTGGCCATATTCGCAAGAGAGGCGGACTGTGCCCTGAGGAG 225  
DB 181 atctggccataatcgcaagagagggcgactgtgccctgaggag 225

RESULT 4  
AAT01166  
ID AAT01166 standard; DNA; 225 BP.  
XX  
XX AAT01166;  
XX  
XX 26-FEB-1996 (first entry)  
XX  
XX MAGE-6 gene.  
XX  
XX MAGE-6; melanoma; tumour rejection antigen; cancer; diagnosis; ss.  
XX  
XX Homo sapiens.  
XX  
XX W09523874-A1.  
XX  
XX 08-SEP-1995.  
XX  
XX 23-FEB-1995; 95WO-US02203.  
XX  
XX 30-NOV-1994; 94US-0346774.  
XX  
XX 01-MAR-1994; 94US-0204727.  
XX  
XX 10-MAR-1994; 94US-0209172.  
XX  
XX 01-SEP-1994; 94US-0299849.  
XX  
XX (LUDW-) LUDWIG INST CANCER RES.  
XX  
XX Boon-Falleur T, Brasseur F, Chomez P, De Plaen E;  
PI De Smet C, Gauglier B, Lethé B, Marchand M, Patard J;  
PI Szikora J, Van Den Eynde B, Van Derbruggen P, Weynants P;  
XX  
XX WPI; 1995-320586/41.  
XX  
XX Determn. of cancerous condition(s) - using a nucleic acid as a  
PT primer to determine expression of a MAGE tumour rejection antigen  
PT precursor  
XX  
XX Example 32; Page 80; 121pp; English.  
XX  
XX A family of human tumour rejection antigen precursor, MAGE, genes  
CC (AAT05091-99, AAT01165-71) was isolated from various tumour cell lines.

CC CDNA (AAT01166) coding for MAGE-6 was obtd. from human melanoma  
CC LB-33-MEL cells. MAGE serve as markers for tumour diagnosis. The  
CC genes are silent in normal cells.  
XX  
XX Sequence 225 BP; 44 A; 56 C; 57 G; 58 T; 0 other;  
SQ

Query Match 99.3%; Score 223.4; DB 16; Length 225;  
Best Local Similarity 99.6%; Pred. No. 9.8e-56;  
Matches 224; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TATTTCTTTCCCTGATCTTCAGCAAGCTTCGGATTCTTCAGCTGCTTTTGGCATT 60  
DB 1 tattttcttcttgatcttcagcaagcttcgattcttcagctgcttttggcattc 60  
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCCTGGCCCTC 120  
DB 61 gagctgatggaagtggaccccatcgccacgtgtacatcttttgccacctgacctggccctc 120  
QY 121 TCCTACGATGGCTGCTGGTGACATTCAGATCATGCCAGGACAGGCTTCCTGTATAATC 180  
DB 121 tctacgatggcctgctggtgacatcagatcatgccagagacaggttctctgataatc 180  
QY 181 ATCTGGCCATATTCGCAAGAGAGGCGGACTGTGCCCTGAGGAG 225  
DB 181 atctggccataatcgcaagagagggcgactgtgccctgaggag 225

RESULT 5  
AAX87596  
ID AAX87596 standard; cDNA; 1362 BP.  
XX  
XX AAX87596;  
XX  
XX 26-OCT-1999 (first entry)  
XX  
XX CLYTA-MAGE-3-His fusion DNA.  
XX  
XX MAGE-3; CLYTA-MAGE-3-His; fusion protein; tumour; melanoma;  
KW breast cancer; bladder cancer; lung cancer; colon cancer;  
KW head and squamous cell carcinoma; oesophagus carcinoma; vaccine;  
KW human; ss.  
XX  
XX Chimeric - Streptococcus pneumoniae.  
XX  
XX Chimeric - Homo sapiens.  
XX  
XX Chimeric - synthetic.  
XX  
XX W09940188-A2.  
XX  
XX 12-AUG-1999.  
XX  
XX 02-FEB-1999; 99WO-EP00660.  
XX  
XX 06-FEB-1998; 98GB-0002650.  
XX  
XX 05-FEB-1998; 98GB-0002543.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
XX Cabezon Silva T, Cohen J, Slaoui MM, Vinals Bassols C;  
PI  
XX WPI; 1999-494293/41.  
XX  
XX P-PSDB; AAY06593.  
XX  
XX New protein derivatives used in cancer vaccine therapy for treating  
PT a range of cancers including melanomas, carcinomas and cancers of  
PT breast  
XX  
XX Example 10; Page 72; 72pp; English.  
XX  
XX This DNA sequence codes for a fusion protein (see AAY06593) composed  
CC of the C-terminal portion of the Streptococcus pneumoniae LYTA  
CC protein (CLYTA), the human MAGE-3 tumour-associated antigen and a  
CC hexahistidine tail. A vector designed for recombinant expression



XX The sequence represents the coding sequence of molecule for disease  
CC detection and treatment, mddt21, shown by computer analysis to be similar  
CC to the MAGE family of proteins. The sequence may be used for  
CC somatic or germline gene therapy. Gene therapy may be performed to: (i)  
CC correct genetic deficiency such as in severe combined immunodeficiency  
CC syndrome associated with adenosine deaminase (ADA) deficiency, cystic  
CC fibrosis, thalassemias, familial hypercholesterolaemia and haemophilia  
CC caused by factor VIII or factor IX deficiencies; (ii) express a  
CC conditional lethal gene product (such as in the case of cancers which  
CC result from unregulated cell proliferation); (iii) express a protein  
CC which affords protection against intracellular parasites (for example,  
CC human retroviruses such as HIV, hepatitis B or C, fungal parasites such  
CC as Candida albicans and Paracoccidioides brasiliensis, and protozoal  
CC parasites such as Plasmodium falciparum and Trypanosoma brasiliensis.  
XX  
SQ Sequence 4204 BP; 947 A; 1145 C; 1219 G; 893 T; 0 other;

Query Match . 97.9%; Score 220.2; DB 22; Length 4204;  
Best Local Similarity 98.7%; Pred. No. 2e-54;  
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 TATTCTTCTTCGTGATCTTCAGCAAGCTTCGGATTCCCTGAGCTGGTCTTTGGCATC 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
2897 tactttctctgtatcttcagcaagcttcgattcctctgcagctggtctttggcatc 2956  
QY 61 GAGCTGATGMAGTGACCCCATCGCCACGCTGACATCTTGGCCACCTGCCCTGGCCCTC 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
2957 gagctgatggaagtggaccccatcgccacgtgtacatctttgccacctgctgggacctc 3016  
QY 121 TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGGCTTCCTGTATAATC 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
3017 tectacgatggcctgctgggtgacaatcagatcatgcccaagacaggtctcctgataatc 3076  
QY 181 ATCCTGGCCATAATCGCAGAGAGGCGGACTGTGCCCTTGAGGAG 225  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
3077 atcttgccataatcgcaaaaggaggcgactgtgccctgaggag 3121

RESULT 8  
AADI2993  
ID AADI2993 standard; DNA; 945 BP.  
XX  
AC AADI2993;  
XX  
DT 16-OCT-2001 (first entry)  
XX  
DE Human MAGE-A3 DNA.  
XX  
KW MAGE antigenic peptide; Human leukocyte antigen; HLA-B35; HLA-B44;  
KW tumour cell; immunostimulant; antigen presentation; cancer; melanoma;  
KW CD8+ cytotoxic T lymphocyte; colorectal; prostate; gastric carcinoma;  
KW myeloma; brain tumour; sarcoma; seminoma; ovarian tumour; cytostatic;  
KW gene therapy; human; MAGE-A3; tumour rejection antigen; TRA; ds.  
XX  
OS Homo sapiens.

XX  
FH Key Location/Qualifiers  
FT CDS 1..945  
FT /\*tag= a  
FT /product= "MAGE-A3 protein"  
XX  
PN WO200153833-A1.  
XX  
PD 26-JUL-2001.  
XX  
PF 19-JAN-2001; 2001WO-US02008.  
XX  
PR 20-JAN-2000; 2000US-0177242.  
PR 25-OCT-2000; 2000US-0243212.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.

XX  
PI Luiten R, Boon-Falleur T, Van Der Bruggen P, Stroobant V;  
Demotte N, Schultz E;  
XX  
DR WPI: 2001-488724/53.  
DR P-PSDB; AAE06853.  
XX  
PT Functional variants and isolated mimetics of a MAGE-A1 HLA-B35 or  
HLA-B44 binding peptide, or of a MAGE-A3 HLA-B35 binding peptide, used  
in diagnosis and treatment of a disorder characterized by expression of  
MAGE-A1 or -A3 -  
XX  
PS Example 3; Page 94-95; 103pp; English.  
XX  
CC The invention relates to functional variants and isolated mimetics of a  
MAGE-A1 human leukocyte antigen (HLA)-B35 or HLA-B44 binding peptide,  
or of a MAGE-A3 HLA-B35 binding peptide, identified by methods described  
in the specification. MAGE genes encode tumour rejection antigens  
(TRAs) presented to T lymphocytes by HLA-B35 and HLA-B44 molecules.  
CC The MAGE antigenic peptide acts by binding to HLA molecules  
on tumour cells and stimulating recognition of these cells and thus  
signalling them to the immune system for destruction. The peptide when  
presented by HLA molecule induces the activation and stimulation of  
CD8+ cytotoxic T lymphocytes. The MAGE antigenic peptide is used to  
treat and diagnose disorders characterised by expression of MAGE-A1  
or -A3. Disorders include cancers e.g melanomas, oesophageal, lung,  
CC head and neck, breast, colorectal, prostate, renal, bladder,  
CC hepatocellular, papillary thyroid and gastric carcinomas, myelomas,  
CC brain tumours, sarcomas, seminomas, and ovarian tumours. The present  
sequence is human MAGE-A3 DNA.  
XX  
SQ Sequence 945 BP; 210 A; 254 C; 278 G; 203 T; 0 other;

Query Match 95.0%; Score 213.8; DB 22; Length 945;  
Best Local Similarity 96.9%; Pred. No. 9.2e-53;  
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 1 TATTCTTCTTCGTGATCTTCAGCAAGCTTCGGATTCCCTGAGCTGGTCTTTGGCATC 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
433 tactttctctgtatcttcagcaagcttcgattcctctgcagctggtctttggcatc 492  
QY 61 GAGCTGATGMAGTGACCCCATCGCCACGCTGACATCTTTCGCCACCTGCCCTGGCCCTC 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
493 gagctgatggaagtggaccccatcgccacgtgtacatctttgccacctgctgggacctc 552  
QY 121 TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGGCTTCCTGTATAATC 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
553 tectacgatggcctgctgggtgacaatcagatcatgcccaagacaggtctcctgataatc 612  
QY 181 ATCCTGGCCATAATCGCAGAGAGGCGGACTGTGCCCTTGAGGAG 225  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
613 gtcttgccataatcgcaaaaggaggcgactgtgccctgaggag 657

RESULT 9  
AAX87592  
ID AAX87592 standard; cDNA; 1212 BP.  
XX  
AC AAX87592;  
XX  
DT 26-OCT-1999 (first entry)  
XX  
DE Haemagglutinin-MAGE-3-His fusion DNA.  
XX  
KW MAGE-3; haemagglutinin; NS1-MAGE-3-His; fusion protein; tumour;  
KW melanoma; breast cancer; bladder cancer; lung cancer;  
KW head and squamous cell carcinoma; colon cancer;  
KW oesophagus carcinoma; vaccine; human; ss.  
XX  
OS Chimeric - Influenza virus.  
OS Chimeric - Homo sapiens.  
OS Chimeric - synthetic.

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XX  WO9940188-A2.
XX  12-AUG-1999.
XX  02-FEB-1999; 99WO-EP00660.
XX  06-FEB-1998; 98GB-0002650.
XX  05-FEB-1998; 98GB-0002543.
XX  (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX  Cabazon Silva T, Cohen J, Slaoui MM, Vinals Bassols C;
XX  WPI; 1999-494293/41.
XX  P-PSDB; AAY06591.
XX  New protein derivatives used in cancer vaccine therapy for treating
XX  a range of cancers including melanomas, carcinomas and cancers of
XX  breast
XX  Example 7; Page 69; 72pp; English.
XX  This DNA sequence codes for a fusion protein (see AAY06591) composed
XX  of haemagglutinin NSI of influenza virus, the human MAGE-3
XX  tumour-associated antigen and a hexahistidine tail. A vector
XX  designed for recombinant expression of the fusion protein is
XX  provided. MAGE-3 cDNA was amplified using primers that altered the
XX  first 5 codons to Escherichia coli codon usage. The NSI moiety
XX  provided the fusion protein with additional exogenous T-helper
XX  epitopes. The invention relates to MAGE proteins fused to an
XX  immunological fusion partner, e.g. NSI-MAGE-3-His. These novel
XX  fusion proteins provide vaccines for immunotherapy of melanomas or
XX  other MAGE-associated tumours like breast, bladder, lung and
XX  non-small cell lung cancer, head and squamous cell carcinoma, colon
XX  carcinoma and oesophagus carcinoma.
XX  Sequence 1212 BP; 289 A; 319 C; 344 G; 260 T; 0 other;

Query Match 95.0%; Score 213.8; DB 20; Length 1212;
Best Local Similarity 96.9%; Pred. No. 1e-52;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCAGCTGCTTGTGGCATC 60
Db 673 tattcttctctgtgatcttcagcaaaagcttcagttccttgcagctggtctttggcattc 732

Qy 61 GAGCTGATGGAAGTGGACCCCGCCACGTGTACATCTTTGCCACCTGCTGGGCCTC 120
Db 733 gagctgatggaagtggaccacctgagccacctgtacatctttgccacctgctgggcctc 792

Qy 121 TCCTACGATGCGCTGCTGGTGCACAAATCAGATCATGCCCCAGACAGGCTTCTGTATATC 180
Db 793 tctacagatggcctgctgggtgacaatcagatcatgcccaggcaggcctcctataatc 852

Qy 181 ATCCTGGCCATAATCGCAAGAGGGCGACTGTGCCCTGAGGAG 225
Db 853 gtcttggccataatcgcaagagaggcgactgtgcccctggagg 897

RESULT 10
AAX87588
ID AAX87588 standard; cDNA; 1353 BP.
XX
AC AAX87588;
XX
XX 26-OCT-1999 (first entry)
XX
XX Lipoprotein D-MAGE-3-His fusion DNA.
XX
XX MAGE-3; lipoprotein D; LPD-MAGE-3-His; fusion protein; tumour;
KW melanoma; breast cancer; bladder cancer; lung cancer;
```

```
KW head and squamous cell carcinoma; colon cancer;
KW oesophagus carcinoma; vaccine; human; ss.
XX
OS Chimeric - Haemophilus influenzae.
OS Chimeric - Homo sapiens.
OS Chimeric - synthetic.
XX
PN WO9940188-A2.
XX
XX 12-AUG-1999.
XX
XX 02-FEB-1999; 99WO-EP00660.
XX
PR 06-FEB-1998; 98GB-0002650.
PR 05-FEB-1998; 98GB-0002543.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Cabazon Silva T, Cohen J, Slaoui MM, Vinals Bassols C;
XX WPI; 1999-494293/41.
XX P-PSDB; AAY06589.
XX
XX New protein derivatives used in cancer vaccine therapy for treating
XX a range of cancers including melanomas, carcinomas and cancers of
XX breast
XX Example 1; Page 66; 72pp; English.
XX This DNA sequence codes for a fusion protein (see AAY06589) composed
XX of lipidated protein D (LPD) of Haemophilus influenzae B, the human
XX MAGE-3 tumour-associated antigen and a hexahistidine tail. A
XX vector designed for recombinant expression of the fusion protein is
XX provided. MAGE-3 cDNA was amplified using primers that altered the
XX first 5 codons to Escherichia coli codon usage. The LPD moiety
XX provided the fusion protein with additional exogenous T-cell
XX epitopes and also increased expression levels in E. coli. The
XX lipid tail ensured optimal presentation of the antigen to
XX antigen-presenting cells. The affinity tag facilitated
XX purification. The invention relates to MAGE proteins fused to an
XX immunological fusion partner, e.g. LPD-MAGE-3-His. These novel
XX fusion proteins provide vaccines for immunotherapy of melanomas or
XX other MAGE-associated tumours like breast, bladder, lung and
XX non-small cell lung cancer, head and squamous cell carcinoma, colon
XX carcinoma and oesophagus carcinoma.
XX
XX Sequence 1353 BP; 342 A; 337 C; 354 G; 320 T; 0 other;

Query Match 95.0%; Score 213.8; DB 20; Length 1353;
Best Local Similarity 96.9%; Pred. No. 1e-52;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCAGCTGCTTGTGGCATC 60
Db 814 tatttcttctctgtgatcttcagcaaaagcttcagttccttgcagctggtctttggcattc 873

Qy 61 GAGCTGATGGAAGTGGACCCCGCCACGTGTACATCTTTGCCACCTGCTGGGCCTC 120
Db 874 gagctgatggaagtggaccacctgagccacctgtacatctttgcccctgggcctc 933

Qy 121 TCCTACGATGCGCTGCTGGTGCACAAATCAGATCATGCCCCAGACAGGCTTCTGTATATC 180
Db 934 tctacagatggcctgctgggtgacaatcagatcatgcccaggcaggcctcctataatc 993

Qy 181 ATCCTGGCCATAATCGCAAGAGGGCGACTGTGCCCTGAGGAG 225
Db 994 gtcttggccataatcgcaagagaggcgactgtgcccctggagg 1038

RESULT 11
AAQ72480
ID AAQ72480 standard; cDNA to mRNA; 1640 BP.
```

XX AAQ72480;  
 AC 22-JUN-1995 (first entry)  
 DT Tumour rejection antigen precursor MAGE-3 cDNA.  
 XX  
 DE Tumour rejection antigen precursor MAGE-3 cDNA.  
 XX  
 KW Tumour antigen rejection precursor; melanoma antigen-3; MAGE-3;  
 KW cancer; cytolytic T cells; antigen D; human leucocyte antigen;  
 KW PIA gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH 172..1116  
 FT /\*tag= a  
 FT  
 XX  
 XX W09423031-A.  
 PN  
 PD 13-OCT-1994.  
 PD  
 PE 17-MAR-1994; 94WO-US02877.  
 PE  
 PR 26-MAR-1993; 93US-0037230.  
 PR  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 XX Boon-falleur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;  
 PI WPI; 1994-333192/41.  
 DR  
 XX New tumour rejection antigen precursor MAGE3 - useful in  
 PT treatment and diagnosis of cancer  
 PT  
 XX  
 XX Example 32; Page 64; 105pp; English.  
 PS  
 XX AAQ72480 is the PIA gene fragment which contains the cDNA coding  
 CC sequence AAQ72470, which encodes melanoma antigen-3 (MAGE-3), a tumour  
 CC rejection antigen precursor. Melanomas characterised by the expression of  
 CC MAGE-3 can be detected, or monitored, by contacting a test sample with  
 CC an agent that can recognise MAGE-3. The melanoma can be treated by the  
 CC administration of cytolytic T cells specific for the complex of  
 CC antigen D (the mature rejection antigen derived from MAGE-3) and a  
 CC human leucocyte antigen (esp. HLA-A1).  
 XX  
 SQ Sequence 1640 BP; 380 A; 402 C; 457 G; 401 T; 0 other;  
 Query Match 95.0%; Score 213.8; DB 15; Length 1640;  
 Best Local Similarity 96.9%; Pred. No. 1.1e-52;  
 Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 TATTCTTCTGATCTTCAGCAAGCTTCGATTCCTTGGGCTTGGGCTC 60  
 Db 604 tattcttctgtgattcttcagcaagcttcgagttcccttgcagctgtgcttggcattc 663  
 QY 61 GAGCTGATGGAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCACCTGCTGGGCTC 120  
 Db 664 gactgatggaagtggaccacctggccacctgtacatctttgccacctgacctgggctc 723  
 QY 121 TCCTACGATGCGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180  
 Db 724 tcctacgatggctgctgggtgacaatcagatcatgcccaaggcaggccctcctgataatc 783  
 QY 181 ATCTGCGCCATATCGCAAGAGGGGCGACTGTGCCCTCGAGGAG 225  
 Db 784 gtctggccataatcgcaagagggcgactgtgccctcgaggag 828  
 RESULT 12  
 AAX84116  
 ID AAX84116 standard; cDNA to mRNA; 1640 BP.  
 DE  
 XX

AC AAX84116;  
 XX 08-SEP-1999 (first entry)  
 DT MAGE-3 gene.  
 XX  
 DE Tumour rejection antigen; vaccine; cancer; MAGE-3 gene; ss.  
 KW  
 XX Homo sapiens.  
 OS  
 XX US925729-A.  
 PN  
 PD 20-JUL-1999.  
 PD  
 PE 02-MAY-1994; 94US-0142368.  
 PE  
 XX 02-MAY-1994; 94US-0142368.  
 PR 23-MAY-1991; 91US-0705702.  
 PR 09-JUL-1991; 91US-0728838.  
 PR 23-SEP-1991; 91US-0764365.  
 PR 12-DEC-1991; 91US-0807043.  
 XX  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 PA  
 XX Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;  
 PI Van Den Eynde B, Van Der Bruggen P, Van Pel A;  
 XX WPI; 1999-418294/35.  
 DR  
 XX New tumour rejection antigen is useful as a vaccine against  
 PT cancerous diseases  
 PT  
 XX Disclosure; Column 51-54; 58pp; English.  
 PS  
 XX This sequence represents the MAGE-3 gene sequence.  
 CC The invention relates to a tumour rejection antigen sequence that is  
 CC useful as a tumour rejection antigen for vaccination against cancerous  
 CC conditions.  
 CC  
 SQ Sequence 1640 BP; 380 A; 402 C; 457 G; 401 T; 0 other;  
 Query Match 95.0%; Score 213.8; DB 20; Length 1640;  
 Best Local Similarity 96.9%; Pred. No. 1.1e-52;  
 Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 TATTCTTCTGATCTTCAGCAAGCTTCGATTCCTTGGGCTTGGGCTC 60  
 Db 604 tattcttctgtgattcttcagcaagcttcgagttcccttgcagctgtgcttggcattc 663  
 QY 61 GAGCTGATGGAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCACCTGCTGGGCTC 120  
 Db 664 gactgatggaagtggaccacctggccacctgtacatctttgccacctgacctgggctc 723  
 QY 121 TCCTACGATGCGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180  
 Db 724 tcctacgatggctgctgggtgacaatcagatcatgcccaaggcaggccctcctgataatc 783  
 QY 181 ATCTGCGCCATATCGCAAGAGGGGCGACTGTGCCCTCGAGGAG 225  
 Db 784 gtctggccataatcgcaagagggcgactgtgccctcgaggag 828  
 RESULT 13  
 AAX26974  
 ID AAX26974 standard; cDNA; 4204 BP.  
 XX  
 XX AAX26974;  
 XX  
 XX 25-JUN-1999 (first entry)  
 DT  
 XX cDNA encoding MAGE-3 polypeptide.  
 DE  
 XX

KW MAGE-3 tumour associated gene; human leukocyte antigen Class II;  
 KW autologous CD4+ cell; MAGE-3 related disease; cancer; melanoma;  
 KW osteosarcoma; leukemia; carcinoma; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH CDS 2465...3409  
 FT /\*tag= a  
 FT /product= "MAGE-3"

XX WO9914326-A1.

XX 25-MAR-1999.

XX 04-SEP-1998; 98WO-US18601.

XX 12-SEP-1997; 97US-0928615.

XX (LUDW-) LUDWIG INST CANCER RES.

XX (UYVR-) UNIV VRIJE BRUSSEL.

XX Boon-Falleur T, Chauv P, Corthals J, Heirman C;

PI Luiten R, Stroobant V, Thielemans K, Van Der Bruggen P;

XX WPI: 1999-244031/20.

DR P-PSDB; AAY01720.

XX Isolated peptides that bind to human leukocyte antigen class II  
 molecules

XX Example 5; Page 65-67; 88pp; English.

XX The present sequence represents the MAGE-3 tumour associated gene.  
 CC Peptides that bind human leukocyte antigen (HLA) class II molecules  
 CC can be derived from the MAGE-3 protein. These peptides and  
 CC autologous CD4+ cells that bind to a complex of MAGE-3 peptide  
 CC and HLA Class II, are used to treat MAGE-3 related diseases,  
 CC particularly cancers (e.g. melanoma, osteosarcoma, leukemia and  
 CC various forms of carcinoma). The peptides are also used to produce  
 CC specific antibodies. Detection of the peptides, e.g. in binding  
 CC assays, particularly with antibodies, is used for diagnosis of such  
 CC diseases.

XX Sequence 4204 BP; 944 A; 1144 C; 1223 G; 893 T; 0 other;

Query Match 95.0%; Score 213.8; DB 20; Length 4204;  
 Best Local Similarity 96.9%; Pred. No. 1.5e-52;  
 Mismatches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTTCTTCTGTCATCTTCAGCAAGCTTCGGATTCTTCAGCTGGTCTTTGGCATC 60  
 DB 2897 tattttcttctgtgtattcttcagcaagcttcagttcttcagctgtgtcttggcattc 2956  
 QY 61 GAGCTGATGGAAGTGGACCCATCGCCACCTGTACATCTTTCAGCTGGCTGCTGGGCTC 120  
 DB 2957 gagctgatggaagtggaccccatcgccactgtacattcttggccactgctgggctc 3016  
 QY 121 TCCTACAGTGGCTGCTGGGTGACAATCAGATCATGCCAGCAGGCTTCTGTATAATC 180  
 DB 3017 tcttacctggtgctgtgtgtgacaatcagatcatgcccaggcagcctcctgataatc 3076  
 QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225  
 DB 3077 gtccctggccataatcgcaagagaggcgactgtgcccctgaggag 3121

RESULT 14

AAA37927

ID AAA37927 standard; cDNA; 4204 BP.

XX AAA37927;

AC AAA37927;

XX

DT

XX

DE

XX

KW

KW

XX

OS

XX

PN

XX

PD

XX

PF

XX

PR

XX

PA

PA

XX

PI

PI

XX

DR

DR

XX

PT

PT

XX

PS

XX

CC

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CC

18-AUG-2000 (first entry)

Human MAGE-A3 nucleotide sequence.

MAGE-A3; HLA class II; human leukocyte antigen; antibody; vaccine;  
 cancer; human; tumour; tumour associated gene product; ss.

Homo sapiens.

WO200020581-A1.

13-APR-2000.

15-SEP-1999; 99WO-US21230.

05-OCT-1998; 98US-0166448.

(LUDW-) LUDWIG INST CANCER RES.

(UYVR-) UNIV VRIJE BRUSSEL.

Chaux P, Stroobant V, Boon-Falleur T, Van Der Bruggen P;

Schultz ES, Van Snick J, Lethe B, Thielemans K, Corthals J;

Heirman C;

WPI: 2000-317713/27.

P-PSDB; AAB02565.

New MAGE-A3 class II binding peptides, useful to diagnose and treat  
 tumours, are fragments of MAGE-A3 which bind to and are presented to T  
 lymphocytes by human leukocyte antigen class II molecules

Example 6; Page 96-98; 119pp; English.

The present invention relates to MAGE-A3 (tumour associated gene  
 product) human leukocyte antigen (HLA) class II-binding peptides (see  
 AAB02566-B02595, and AAB02633-B02637). These peptides are presented to T  
 cells in the context of HLA class II molecules. The peptides stimulate  
 the activity and proliferation of CD4+ T lymphocytes. The invention also  
 includes nucleotide sequences encoding MAGE-3A peptides (see AAA37928  
 and AAA37938-A37940). The peptides and nucleotide sequences can be used  
 to create antibodies against the MAGE-A3 peptides, the antibodies,  
 peptides and nucleotide sequences can be used to create a vaccine. The  
 peptides are used to diagnose or treat a disorder characterized by  
 expression of MAGE-3, particularly cancer. The methods can also be used  
 in the diagnosis of disorders associated with MAGE-3 expression. Included  
 in the invention are other human tumour antigens (see AAB02596-B02637),  
 and PCR primers used in the course of the invention (see AAA37929-A37937  
 and AAA37941-A37942).

Sequence 4204 BP; 944 A; 1144 C; 1223 G; 893 T; 0 other;

Query Match 95.0%; Score 213.8; DB 21; Length 4204;  
 Best Local Similarity 96.9%; Pred. No. 1.5e-52;  
 Mismatches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTTCTTCTGTCATCTTCAGCAAGCTTCGGATTCTTCAGCTGGTCTTTGGCATC 60  
 DB 2897 tattttcttctgtgtattcttcagcaagcttcagttcttcagctgtgtcttggcattc 2956  
 QY 61 GAGCTGATGGAAGTGGACCCATCGCCACCTGTACATCTTTCAGCTGGCTGCTGGGCTC 120  
 DB 2957 gagctgatggaagtggaccccatcgccactgtacattcttggccactgctgggctc 3016  
 QY 121 TCCTACAGTGGCTGCTGGGTGACAATCAGATCATGCCAGCAGGCTTCTGTATAATC 180  
 DB 3017 tcttacctggtgctgtgtgtgacaatcagatcatgcccaggcagcctcctgataatc 3076  
 QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225  
 DB 3077 gtccctggccataatcgcaagagaggcgactgtgcccctgaggag 3121



Db	724	tcctacgatggcctgctgggtgacaatcagatcatgccaaagcaggcctcctgataatc	783
QY	181	ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTCAGGAG	225
Db	784	gtcctggccataatcgcgaagagggcactgtgccctgaggag	828

Search completed: December 4, 2001, 12:19:28  
Job time: 3011 sec

melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen; tumor rejection antigen precursor; MAGE; antigen E; gene family; ss.

**Homo sapiens.**

Key	Location/Qualifiers
CDS	172..1116
	/*tag= a

WO9220356-A.

26-NOV-1992.

22-MAY-1992: 92WO-US04354.

23-MAY-1991: 91US-0705702.

09-JUL-1991; 91US-0728838.

23-SEP-1991; 91US-0764364.

12-DEC-1991; 91US-0807043.

(LUDW-) LUDWIG INST CANCER RES.

Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;

Van Den Eynde B, Van Der Bruggen P, Van Pel A;

WPI; 1992-415460/50.

Nucleic acid mol. encoding a human tumour rejection antigen precursor - useful as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis

Disclosure; Page 77; 142pp; English.

The sequences given in AAQ32352-69 represent a new family of genes referred to as melanoma antigens (MAGE). The cDNAs of this gene family were identified during the isolation of the antigen E gene. The MAGE cDNAs, when tested, did not transfer expression of antigen E, but they did show substantial homology to the antigen E cDNA sequence. The MAGE DNAs share a certain degree of homology with each other and are expressed in tumour cells including several types of human tumor cells as well as in human tumors. MAGE expression is not restricted to melanomas. MAGE refers to a family of tumor rejection antigen precursors. The antigens resulting from these genes are referred to as MAGE TRAs or melanoma antigen tumor rejection antigens. See also AAQ32351.

Sequence 1640 BP; 379 A; 395 C; 465 G; 401 T; 0 other;

Query Match 94.3%; Score 212.2; DB 13; Length 1640;  
Best Local Similarity 96.4%; Pred. No. 3.2e-52;  
Matches 217; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy	1	TATTTCTTTCCTGTGATCTTCAGCAAAGCTTCCGATTCCCTTGCAAGCTGGTCTTTTGGCATC	60
Db	604	tattttcttctgtgatttcagcaaaagcttcacagtctccttgacgtggtctttggcatg	663

QY 61 GAGTGTGGAAGTGGACCCCATGGCCACGTTACATCTTTGCCACCTGGCTGGGCTC 120

Db 664 gagctgatggaagtggaccccatcgccacttgtagcatcttggcacctgacctgggcctc 723

Qy 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180





MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: MAGE-6 gene

Initial Score = 225 Optimized Score = 225 Significance = 1.46  
Residue Identity = 100% Matches = 225 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

X 10 20 30 40 50 60 70  
TATTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTGGCAGCTGGTCTTGGCAGCTGATGAA  
|||||  
TATTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTGGCAGCTGGTCTTGGCAGCTGATGAA  
X 10 20 30 40 50 60 70

GTGACCCATCGCCACGCTGATCATCTTCCACCTGCTGGCCCTCTCTAGATGGCTGCTGGTGAC  
80 90 100 110 120 130 140  
GTGACCCATCGCCACGCTGATCATCTTCCACCTGCTGGCCCTCTCTAGATGGCTGCTGGTGAC  
80 90 100 110 120 130 140

AATCAGATCATGCCACGAGCTTCTCTGATATCATCTTGGCCATAATCGCAAGAGGGGACTGTGCC  
150 160 170 180 190 200 210  
AATCAGATCATGCCACGAGCTTCTCTGATATCATCTTGGCCATAATCGCAAGAGGGGACTGTGCC  
150 160 170 180 190 200 210

220 X  
CCTGAGGAG  
|||||  
CCTGAGGAG  
220 X

2. US-08-037-230D-18 (1-225)  
US-07-807-043B-1 Sequence 11, Application US/07807043B

Sequence 11, Application US/07807043B

Patent No. 5342774

GENERAL INFORMATION:

APPLICANT: Boon, Thierry, Van den Eynde, Beno t  
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor  
TITLE OF INVENTION: Rejection Antigens and Uses thereof

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felife & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/807,043B

FILING DATE: 19911212

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/764,364

FILING DATE: 23-SEPTEMBER-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/728,838

FILING DATE: 9-JULY-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/705,702

FILING DATE: 23-May-1991

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 5342774man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 253.3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 1640 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: singular

TOPOLOGY: linear

MOLECULE TYPE: CDNA to mRNA

FEATURE:

NAME/KEY: CDNA MAGE-3

Initial Score = 218 Optimized Score = 218 Significance = 1.38  
Residue Identity = 96% Matches = 218 Mismatches = 7  
Gaps = 0 Conservative Substitutions = 0

AGCCGGTCACAAAGGAGAAATCTCGGGAGTGTCTCGGAAATTTGGCAGTATTTCTTCTCTGTGATCTTCA  
560 570 580 590 600 610 620  
X 10 20  
TATTCTTCTCTGTGATCTTCA  
|||||

GCAAGCTTCGATTTCTTTCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCATCGCCACGCTGT  
30 40 50 60 70 80 90  
GCAAGCTTCGATTTCTTTCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCATCGCCACGCTGT  
30 40 50 60 70 80 90

ACATCTTTGGCAGCTGCTGGGCTCTCTTACGATGGCTGCTGGGTGACAATCAGATCATGCCCAGGACAG  
100 110 120 130 140 150 160  
ACATCTTTGGCAGCTGCTGGGCTCTCTTACGATGGCTGCTGGGTGACAATCAGATCATGCCCAGGACAG  
100 110 120 130 140 150 160

GCCTCTGATAATCGTCTGCTGCCATATCGCAAGAGAGGGGAGTGTGCCCCCTGAGGAGGAGGAGGAGG  
170 180 190 200 210 220 X  
GCCTCTGATAATCGTCTGCTGCCATATCGCAAGAGAGGGGAGTGTGCCCCCTGAGGAGGAGGAGGAGGAGG  
170 180 190 200 210 220 X

AGCTGAGTGTGTTAGAGGCTTTTTCAGGGGAGGGAAGA  
850 860 870

3. US-08-037-230D-18 (1-225)  
US-07-807-043B-9 Sequence 9, Application US/07807043B

Sequence 9, Application US/07807043B

Patent No. 5342774

GENERAL INFORMATION:

APPLICANT: Boon, Thierry, Van den Eynde, Beno t  
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor

TITLE OF INVENTION: Rejection Antigens and Uses thereof

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felife & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/807,043B

FILING DATE: 19911212

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/764,364

FILING DATE: 23-SEPTEMBER-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/728,838

ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS

GENERAL INFORMATION:  
APPLICANT: Boon, Thierry, Van den Eynde, Beno t  
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor  
TITLE OF INVENTION: Rejection Antigens and Uses Thereof  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch

Sequence 13, Application US/07807043B  
Patent No. 5342774  
GENERAL INFORMATION:  
APPLICANT: Boon, Thierry, Van den Eynde, Beno t  
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor  
TITLE OF INVENTION: Rejection Antigens and Uses Thereof  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fefre & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/807,043B  
FILING DATE: 19911212  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/764,364  
FILING DATE: 23-SEPTEMBER-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/728,838  
FILING DATE: 9-JULY-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/705,702  
FILING DATE: 23-May-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5342774man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 253.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1067 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: singular  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: cDNA MAGE-4

[illegible]

[illegible]









US-07-807-043B-2 Sequence 2, Application US/07807043B

Sequence 2, Application US/07807043B

Patent No. 5342774

GENERAL INFORMATION:

APPLICANT: Boon, Thierry, Van den Eynde, Beno t  
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor  
TITLE OF INVENTION: Rejection Antigens and Uses Thereof  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/807,043B

FILING DATE: 19911212

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/764,364

FILING DATE: 23-SEPTEMBER-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/728,838

FILING DATE: 9-JULY-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/705,702

FILING DATE: 23-May-1991

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 5342774man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 253.3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-3884

TELEFAX: (212) 688-9200

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 675 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: singular

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

Initial Score = 24 Optimized Score = 59 Significance = -0.85  
Residue Identity = 47% Matches = 71 Mismatches = 63  
Gaps = 15 Conservative Substitutions = 0

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ATGCTCTGATAAC-AAAGAAACCA  
X  
10 20

110 120 130 140 150 160 170  
GCCTGGGCTCTTCCTACGATGGCTGTG--GGTGA---CAATCAGATC-ATGCCACAGACAGG--CTTCCT  
|||||  
GACAAAGCC-CACAGTGGCTCAGGTGGTGACGGTGTGGAATAGGTGCAATTTATTGACCGGTACTCCCT  
30 40 50 60 70 80 90

180 190 200 210 220 X  
GATAATCATCTGGCCATA-ATCGCAAGAGAGGGC--GACTGTGCCCTGAGGAG  
|||||  
GGAAGAAATTC-T-GCCTATCTAGGTGGTGTCTTCGCTGTGTGTCACAAAGAGTTTCTGGCGCTCCAGA  
100 110 120 130 140 X 150 160

TGTTTCATAGACGCCCTTTATGAGGACAGTAGT  
170 180 190

15. US-08-037-230D-18 (1-225)

US-07-807-043B-3 Sequence 3, Application US/07807043B

Sequence 3, Application US/07807043B

Patent No. 5342774

GENERAL INFORMATION:

APPLICANT: Boon, Thierry, Van den Eynde, Beno t  
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor  
TITLE OF INVENTION: Rejection Antigens and Uses Thereof  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/807,043B

FILING DATE: 19911212

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/764,364

FILING DATE: 23-SEPTEMBER-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/728,838

FILING DATE: 9-JULY-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/705,702

FILING DATE: 23-May-1991

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 5342774man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 253.3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 228 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: singular

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

Initial Score = 11 Optimized Score = 68 Significance = -1.00  
Residue Identity = 44% Matches = 77 Mismatches = 85  
Gaps = 12 Conservative Substitutions = 0

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CTTTCCTGTGATCTTTCAGCAAGCTTCCGATTCCTTGCGAGCTGGTCTTTGGCATCGAGCTG--ATG-GAAGT  
|||||  
GCATCGAGTTGCAAGGCCGAGA  
X  
10 20

80 90 100 110 120 130 140  
GGACCCCATCGGCCACGCTGTACATCTTTGCCACCTGCGCTGGCCCTCTCCTAGGATGGCTGCTGGGTGACAA  
|||||  
AGAAAGAAATGGACA-GCGGA-AGAAGTGGTGTGTTTTTTTCCCTTCATTAATTTCTAGTTTCTAGTAA  
30 40 50 60 70 80 90

150 160 170 180 190 200 210  
T-CACATCATGCCACGAGCAGAGCTTCCTGATATCATCTGCGCATTAATCGCAAGAGAGGCGGCTGTGCC  
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TCCAGAAAT----TTGATTTGTT-CTAAAGTTTCTATTAT-GCAAGATGTCACCAACAGACTTCTGACTGC  
100 110 120 130 140 150

220 X

CTGAGGAG  
||  
ATGCTGAACCTTCATATGATACATAGGATTACACTTGTACCTGTCTTAAAAATAAAAGTT  
160 X 170 180 190 200 210

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 4, 2001, 09:45:42 : Search time 1322.08 Seconds  
(without alignments)  
2807.595 Million cell updates/sec

Title: US-08-037-230D-18  
Perfect score: 225  
Sequence: 1 TATTTCCTTCCTGTGATCTT.....GCGACTGTGCCCTGAGGAG 225

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vl.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_om.\*  
20: em\_or.\*  
21: em\_ov.\*  
22: em\_pat.\*  
23: em\_ph.\*  
24: em\_pl.\*  
25: em\_ro.\*  
26: em\_sts.\*  
27: em\_sy.\*  
28: em\_un.\*  
29: em\_vl.\*  
30: em\_htgo\_hum.\*  
31: em\_htgo\_inv.\*  
32: em\_htgo\_rod.\*  
33: em\_htg\_hum.\*  
34: em\_htg\_inv.\*  
35: em\_htg\_rod.\*  
36: em\_htg\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	225	100.0	225	6	ARI53509	ARI53509 Sequence
2	225	100.0	225	6	I36933	I36933 Sequence 18
3	220.2	97.9	945	9	HSU10339	U10339 Human MAGE-
4	220.2	97.9	1019	9	HUMMAGEB	D32076 Human mRNA
5	220.2	97.9	1362	6	AX019384	AX019384 Sequence
6	220.2	97.9	3871	9	HSU10691	U10691 Human MAGE-
7	220.2	97.9	245077	9	AF002997	AF002997 Homo sapi
8	213.8	95.0	1212	6	AX019380	AX019380 Sequence
9	213.8	95.0	1353	6	AX019376	AX019376 Sequence
10	213.8	95.0	1640	6	ARI53502	ARI53502 Sequence
11	213.8	95.0	1640	6	I36926	I36926 Sequence 11
12	213.8	95.0	1663	9	BC011744	BC011744 Homo sapi
13	213.8	95.0	1709	9	BC000340	BC000340 Homo sapi
14	213.8	95.0	1753	9	BC005963	BC005963 Homo sapi
15	213.8	95.0	4204	6	AR079453	AR079453 Sequence
16	213.8	95.0	4204	9	HSU03735	U03735 Human MAGE-
17	213.8	95.0	245077	9	AF002997	AF002997 Homo sapi
18	213.8	95.0	289248	9	U82671	U82671 Homo sapien
19	196.8	87.5	1678	9	BC003408	BC003408 Homo sapi
20	195.2	86.8	4157	6	ARI53500	ARI53500 Sequence
21	195.2	86.8	4157	6	I36924	I36924 Sequence 9
22	195.2	86.8	4523	6	AX119704	AX119704 Sequence
23	195.2	86.8	4523	9	HUMMAGE12X	L18877 Human MAGE-
24	195.2	86.8	4559	9	HUMMAGE2X	L18920 Human MAGE-
25	195.2	86.8	289248	9	U82671	U82671 Homo sapien
26	192	85.3	15260	2	AC084372	AC084372 Homo sapi
27	163.2	72.5	1084	6	AR052774	AR052774 Sequence
28	163.2	72.5	1094	6	AR052773	AR052773 Sequence
29	163.2	72.5	1338	6	AX019382	AX019382 Sequence
30	163.2	72.5	1341	6	AX019377	AX019377 Sequence
31	163.2	72.5	1624	6	AX060181	AX060181 Sequence
32	163.2	72.5	2419	6	ARI53498	ARI53498 Sequence
33	163.2	72.5	2419	6	I36922	I36922 Sequence 7
34	163.2	72.5	2420	6	AR007331	AR007331 Sequence
35	163.2	72.5	2420	9	HUMMAG1A	M77481 Human antig
36	163.2	72.5	5674	6	AR060975	AR060975 Sequence
37	163.2	72.5	5674	6	ARI53499	ARI53499 Sequence
38	163.2	72.5	5674	6	I24013	I24013 Sequence 1
39	163.2	72.5	5674	6	I36923	I36923 Sequence 8
40	163.2	72.5	275159	9	U82670	U82670 Homo sapien
41	159.6	70.9	954	9	HSU10340	U10340 Human MAGE-
42	159.6	70.9	1022	9	HUMMAGEA	D32075 Human mRNA
43	159.6	70.9	1022	9	HUMMAGEC	D32077 Human mRNA
44	159.6	70.9	2531	6	ARI53505	ARI53505 Sequence
45	159.6	70.9	2531	6	I36929	I36929 Sequence 14

ALIGNMENTS

RESULT 1  
ARI53509  
LOCUS ARI53509 225 bp DNA  
DEFINITION Sequence 18 from patent US 6235525.  
ACCESSION ARI53509 PAT  
VERSION ARI53509.1 GI:15121041  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 225)  
AUTHORS van den Eynde,B., van der Bruggen,P. and Boon-Falleur,T.  
TITLE Isolated nucleic acid molecules coding for tumor rejection antigen precursor MAGE-3 and uses thereof  
JOURNAL Patent: US 6235525-A 18 22-MAY-2001;  
FEATURES Location/Qualifiers  
source 1..225  
BASE COUNT 44 a 65 c 58 g 58 t  
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Best Local Similarity 100.0%; Pred. No. 1.9e-43;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCAGATTCCTTGCAGCTGGTCTTTGGCATC 60
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Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTTGGCACCTGCCTGGGCCTC 120
Db 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTTGGCACCTGCCTGGGCCTC 120

Qy 121 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCCCAGGACAGGCTTCCTGATAATC 180
Db 121 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCCCAGGACAGGCTTCCTGATAATC 180

Qy 181 ATCCTGGCCATAATCGCAAGAGAGGGGACGTGTGCCCTGAGGAG 225
Db 181 ATCCTGGCCATAATCGCAAGAGAGGGGACGTGTGCCCTGAGGAG 225

RESULT 2
LOCUS I36933 225 bp DNA PAT 13-MAY-1997
DEFINITION Sequence 18 from patent US 5612201.
ACCESSION I36933
VERSION I36933.1 GI:2084893
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 225)
AUTHORS De Plaen,E., Boon-Falleur,T., Lethe ,B., Szkiora,J., De Smet,C. and Chomez,P.
TITLE Isolated nucleic acid molecules useful in determining expression of a tumor rejection antigen precursor
JOURNAL Patent: US 5612201-A 18 18-MAR-1997;
FEATURES
source 1..225
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BASE COUNT 44 a 65 c 58 g 58 t
ORIGIN

Query Match      100.0%; Score 225; DB 6; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.9e-43;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCAGATTCCTTGCAGCTGGTCTTTGGCATC 60
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Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTTGGCACCTGCCTGGGCCTC 120
Db 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTTGGCACCTGCCTGGGCCTC 120

Qy 121 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCCCAGGACAGGCTTCCTGATAATC 180
Db 121 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCCCAGGACAGGCTTCCTGATAATC 180

Qy 181 ATCCTGGCCATAATCGCAAGAGAGGGGACGTGTGCCCTGAGGAG 225
Db 181 ATCCTGGCCATAATCGCAAGAGAGGGGACGTGTGCCCTGAGGAG 225

RESULT 3
LOCUS HSU10339 945 bp mRNA PRI 13-JUN-1994
DEFINITION Human MAGE-3b mRNA, complete cds.
ACCESSION U10339
VERSION U10339.1 GI:499121
```

```
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 945)
AUTHORS Fenton,R.G.
TITLE Cloning and Analysis of MAGE-1 Related Genes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 945)
AUTHORS Fenton,R.G.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-1994) Robert G. Fenton, BRMP, NCI-FCRDC,
Frederick, MD 21702, USA
FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
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/haplotype="HLA-A1/A2"
/cell_line="DM150"
/cell_type="melanoma"
/tissue_type="skin"
/dev_stage="adult"
/clone_lib="DM150 library"
/notes="cancer patient"
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/product="MAGE-3b"
/protein_id="AAAI9006.1"
/db_xref="GI:499122"
/translation="MPLEQRSHQKPEEGLEARGEALGLVGAQAPATEQEAAASSST
LVEVTLGEVPAAESPPPOSQASLPTTMNYPWSQSYEDSSNOEEGSPFPDLE
SEQAALSRKVAKLHFLLLKYRAREPVTKAEMGLSVGNWQYFFVFESKASDSLQL
VFGEIEMVDPIGHVYIFATCLGSLDGLLDNQIMPFGFLIIILAIIAKEGDCAPE
EKIWEELSVLEVEFEGREDSIFGDPKKLLTQYFVOENLYEYRQVFGSDPACYEFWGPFR
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BASE COUNT 213 a 254 c 275 g 203 t
ORIGIN

Query Match      97.9%; Score 220.2; DB 9; Length 945;
Best Local Similarity 98.7%; Pred. No. 2.2e-42;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATC 60
Db 433 TACTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATC 492

Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120
Db 493 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 552

Qy 121 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCCCAGGACAGGCTTCCTGATAATC 180
Db 553 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCCCAGGACAGGCTTCCTGATAATC 612

Qy 181 ATCCTGGCCATAATCGCAAGAGAGGGGACGTGTGCCCTGAGGAG 225
Db 613 ATCCTGGCCATAATCGCAAGAGAGGGGACGTGTGCCCTGAGGAG 657

RESULT 4
LOCUS HUMMAGEB 1019 bp mRNA PRI 07-FEB-1999
DEFINITION Human mRNA for MAGE-6 protein, complete cds.
ACCESSION D32076
VERSION D32076.1 GI:1125015
KEYWORDS MAGE-6 protein; melanoma antigen.
SOURCE Homo sapiens cell-line M73 cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
```

REFERENCE 1 (bases 1 to 1019)  
AUTHORS Imai,Y.  
TITLE Direct Submission  
JOURNAL Submitted (08-JUL-1994) to the DDBJ/EMBL/GenBank Databases.  
Yasuhisa Imai, Kurume University School of Medicine, Immunology;  
Asahi 67, Kurume, Fukuoka 830, Japan (Tel:0942-31-7551,  
Fax:10942-31-7699)  
REFERENCE 2 (bases 1 to 1019)  
AUTHORS Imai,Y., Shichijo,S., Yamada,A., Katayama,T., Yano,H. and Itoh,K.  
TITLE Sequence analysis of the MAGE gene family encoding human  
tumor-rejection antigens  
JOURNAL Gene 160 (2), 287-290 (1995)  
MEDLINE 95369706  
FEATURES  
source Location/Qualifiers  
1..1019  
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/standard\_name="melanoma antigen-6"  
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27 nucleotide sequences of HLA-A1 binding motif (Traversari  
etc., 1992)"  
/codon\_start=1  
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LVEVLGVPAESDPQSPQASLPFTMYPLMSQSYEDSSNOEEGPTFDLE  
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VEGIELMDPDIYHIFATCLGLSDGLDGNQIMPTGFLIIILAIKRGDCAPE  
EKIWEVLVEFEGREDSIFGDPKLLTQVFOENYLEYRQVPGSDPACYEFLWGP  
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BASE COUNT 224 a 284 c 292 g 219 t  
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Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 558 GAGCTGATGGAAGTGGACCCATCGCCAGCTGTACATCTTTGCCACCTGCCTGGGCCTC 617  
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Db 618 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGCTTCCTGTATAATC 677  
QY 181 ATCTTGCCATATTCGCAAGAGGGCGACTGTGCCCTCGAGGAG 225  
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Db 678 ATCTTGCCATATTCGCAAGAGGGCGACTGTGCCCTCGAGGAG 722

RESULT 5  
AX019384  
LOCUS AX019384 1362 bp DNA PAT 07-SEP-2000  
DEFINITION Sequence 10 from Patent WO9940188.  
ACCESSION AX019384  
VERSION AX019384.1 GI:10043354  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1362)  
AUTHORS Slaoui,M.M., Cohen,J., Cabezon,S.T. and Vinals,B.C.  
TITLE Tumor-associated antigen derivatives from the mage family, and

nucleic acid sequences encoding them, used for the preparation of  
fusion proteins and of compositions for vaccination  
Patent: WO 9940188-A 10 12-AUG-1999;  
SLAOUI MONCEF MOHAMED (BE); SMITHKLINE BEECHAM BIOLOG (BE); COHEN  
JOSEPH (BE); CABEZON SILVA TERESA (BE); VINALS BASSOLS CARLOTA (BE)  
Location/Qualifiers  
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Best Local Similarity 98.7%; Pred. No. 2.1e-42;  
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 6  
HSU10691  
LOCUS HSU10691 3871 bp DNA PRI 23-JUN-1995  
DEFINITION Human MAGE-6 antigen (MAGE6) gene, complete cds.  
ACCESSION U10691  
VERSION U10691.1 GI:533522  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 3871)  
AUTHORS De Plaen,E., Arden,K., Traversari,C., Gaforio,J.J., Szikora,J.P.,  
De Smet,C., Brasseur,F., van der Bruggen,P., Lethe,B., Lurquin,C.,  
Brasseur,R., Chomez,P., De Backer,O., Cavenee,W. and Boon,T.  
TITLE Structure, chromosomal localization, and expression of 12 genes of  
the MAGE family  
JOURNAL Immunogenetics 40 (5), 360-369 (1994)  
MEDLINE 95012457  
REFERENCE 2 (bases 1 to 3871)  
AUTHORS De Plaen,E.  
TITLE Direct Submission  
JOURNAL Submitted (14-JUN-1994) Etienne De Plaen, Ludwig Institute for  
Cancer Research, 74 Avenue Hippocrate, Brussels, 1200, Belgium  
FEATURES  
source Location/Qualifiers  
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DEFINITION			
ACCESSION			
VERSION			
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AUTHORS			
TITLE			
JOURNAL			
FEATURES			
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Qy	61	GAGCTGATGGAAGTGAGCCCAATCGGCCACGTGTACATCTTTGCCACCTGCCCTGGGCCTC	120
Db	733	GAGCTGATGGAAGTGAGCCCAATCGGCCACGTGTACATCTTTGCCACCTGCCCTGGGCCTC	792
Qy	121	TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGGCTTCCTGTATAATC	180
Db	793	TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGGCTTCCTGTATAATC	852
Qy	181	ATCTGGCCATATCCACAGAGAGGCGGACTGTGCCCTGAGGAG	225
Db	853	GTCTGGCCATATCCACAGAGAGGCGGACTGTGCCCTGAGGAG	897
RESULT 9			
AX019376			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
1..1353			
/organism="Homo sapiens"			
/db_xref="taxon:9606"			
/note="Melanoma tissue"			
BASE COUNT		342 a	320 t
ORIGIN			
Query Match			
Best Local Similarity 95.0%; Score 213.8; DB 6; Length 1353;			
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;			
Qy	1	TATTTCTTCTGTGATCTTCAGAAAGCTTCGATTCCTTCAGCTGGTCTTTGGCATC	60
Db	814	TATTTCTTCTGTGATCTTCAGAAAGCTTCGATTCCTTCAGCTGGTCTTTGGCATC	873
Qy	61	GAGCTGATGGAAGTGAGCCCAATCGGCCACGTGTACATCTTTGCCACCTGCCCTGGGCCTC	120
Db	874	GAGCTGATGGAAGTGAGCCCAATCGGCCACGTGTACATCTTTGCCACCTGCCCTGGGCCTC	933
Qy	121	TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGGCTTCCTGTATAATC	180
Db	934	TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGGCTTCCTGTATAATC	993
Qy	181	ATCTGGCCATATCCACAGAGAGGCGGACTGTGCCCTGAGGAG	225

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QY 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCAGATTCTTCAGCTGCTGCTTTGGCATC 60
Db 604 TATTTCTTCTGTGATCTTCAGCAAGCTTCAGATTCTTCAGCTGCTGCTTTGGCATC 663
QY 61 GAGCTGATGGAAGTGGACCCATCGCCACGCTGATACATCTTTGCCACCTGCTGGGCCTC 120
Db 664 GAGCTGATGGAAGTGGACCCATCGCCACCTGATACATCTTTGCCACCTGCTGGGCCTC 723
QY 121 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCCCAGCAGGCTTCTGTGATAATC 180
Db 724 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCCCAGCAGGCTTCTGTGATAATC 783
QY 181 ATCCTGGCCATAATCGCAAGAGAGCGGCTGCTGCCCTGAGGAG 225
Db 784 GTCCCTGGCCATAATCGCAAGAGAGCGGCTGCTGCCCTGAGGAG 828

RESULT 12
BC011744
LOCUS BC011744 1663 bp mRNA PRI 02-AUG-2001
DEFINITION Homo sapiens, Similar to melanoma antigen, family A, 3, clone
MGC:19667 IMAGE:3345801, mRNA, complete cds.
ACCESSION BC011744
VERSION BC011744.1 GI:15079897
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1663)
Strausberg, R.
Direct Submission
Submitted (30-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapps-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ruben Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, Q.L., Masello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
Tongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 27 Row: b Column: 12
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.
FEATURES
Location/Qualifiers
1. .1663
/db_xref="taxon:9606"
/clone="MGC:19667 IMAGE:3345801"
/tissue_type="Skin, melanotic melanoma."
/clone_lib="NIH_MGC_20"
/lab_host="DH10B-R"
/note="vector: pOTB7"
145. .1089
/codon_start=1
/product="Similar to melanoma antigen, family A, 3"

CDS
FEATURES
source
1. .1663
/db_xref="taxon:9606"
/clone="MGC:19667 IMAGE:3345801"
/tissue_type="Skin, melanotic melanoma."
/clone_lib="NIH_MGC_20"
/lab_host="DH10B-R"
/note="vector: pOTB7"
145. .1089
/codon_start=1
/product="Similar to melanoma antigen, family A, 3"

Query Match 95.08; Score 213.8; DB 9; Length 1663;
Best Local Similarity 96.9%; Pred. No. 6.7e-41;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCAGATTCTTCAGCTGCTGCTTTGGCATC 60
Db 577 TATTTCTTCTGTGATCTTCAGCAAGCTTCAGATTCTTCAGCTGCTGCTTTGGCATC 636
QY 61 GAGCTGATGGAAGTGGACCCATCGCCACGCTGATACATCTTTGCCACCTGCTGGGCCTC 120
Db 637 GAGCTGATGGAAGTGGACCCATCGCCACCTGATACATCTTTGCCACCTGCTGGGCCTC 696
QY 121 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCCCAGCAGGCTTCTGTGATAATC 180
Db 697 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCCCAGCAGGCTTCTGTGATAATC 756
QY 181 ATCCTGGCCATAATCGCAAGAGAGCGGCTGCTGCCCTGAGGAG 225
Db 757 GTCCCTGGCCATAATCGCAAGAGAGCGGCTGCTGCCCTGAGGAG 801

RESULT 13
BC000340
LOCUS BC000340 1709 bp mRNA PRI 12-JUL-2001
DEFINITION Homo sapiens, melanoma antigen, family A, 3, clone MGC:8564
IMAGE:2822978, mRNA, complete cds.
ACCESSION BC000340
VERSION BC000340.1 GI:12653144
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1709)
Strausberg, R.
Direct Submission
Submitted (15-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapps-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ruben Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, Q.L., Masello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
Tongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
```

Series: IRAL Plate: 1 Row: k Column: 3  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 7280331.

## FEATURES

## source

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1. .1709
/organism="Homo sapiens"
/db_xref="LocusID:4102"
/db_xref="taxon:9606"
/clone="MGC:8564 IMAGE:2822978"
/tissue_type="lung, small cell carcinoma"
/clone_lib="NIH_MGC_7"
/lab_host="DH10B-R"
/notes="Vector: pORB7"
184. .1128
/codon_start=1
/product="melanoma antigen, family A, 3"
/protein_id="AAH0340.1"
/db_xref="GI:12653145"
/translation="MPLEQRSHCKPEEGLEARGALGLVGAQAPATEEEQEAASSST
LVEVTIGVPAAESDPQSGASLPTTMYPLWSQSYEDSSNOEEGSPSTFPDLE
SEFQAALSRKVAELVHLLKYRAREPVTKAEMLGSVGNWQYFPFVIFSKASSLQLE
VFGIELMEVDPIGHLYIFATCLGLSYDGLGDNOIMPKAGLLIIVLAIAREGDCAPE
EKINELSVLEVFEGRESILGDPKLLTQHVFQENYLEYRQVPSDPAFYELWGPGR
ALVETSYVKLVHMHMKISGPHISYPPLHEWVLRGEE"
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## BASE COUNT

422 a 408 c 468 g 411 t

## ORIGIN

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Query Match 95.0%; Score 213.8; DB 9; Length 1709;
Best Local Similarity 96.9%; Pred. No. 6.7e-41;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTTCTTCTTGATCTTCAGCAAGCTTCGATTCCTTGCGAGCTGGTCTTTGGCATC 60
Db 616 TATTTCTTCTTGATCTTCAGCAAGCTTCGATTCCTTGCGAGCTGGTCTTTGGCATC 675

QY 61 GAGCTGATGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCCTGGGCCCTC 120
Db 676 GAGCTGATGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCCTGGGCCCTC 735

QY 121 TCCTAGCATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCCTGTGATAATC 180
Db 736 TCCTAGCATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCCTGTGATAATC 795

QY 181 ATCTCGGCATATTCGCAAGAGGGCGACTGTGCCCTGAGGAG 225
Db 796 GTCTGGCCATATTCGCAAGAGGGCGACTGTGCCCTGAGGAG 840
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## RESULT 14

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BC005963
LOCUS BC005963 1753 bp mRNA PRI 12-JUL-2001
DEFINITION Homo sapiens, melanoma antigen, family A, 3, clone MGC:14613
IMAGE:4064879, mRNA, complete cds.
ACCESSION BC005963
VERSION BC005963.1 GI:13543626
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
Strausberg, R.
Direct Submission
Submitted (02-APR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cdna Library Preparation: CLONTECH Laboratories, Inc.
```

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www.shgc.stanford.edu>  
Contact: (Dickson, Mark) mcdpaxil.stanford.edu  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
R. M.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 21 Row: a Column: 13  
This clone was selected for full length sequencing because it  
passed the following selection criteria: Similarity but not  
identity to protein.

## FEATURES

## Location/Qualifiers

## source

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1. .1753
/organism="Homo sapiens"
/db_xref="LocusID:4102"
/db_xref="taxon:9606"
/clone="MGC:14613 IMAGE:4064879"
/tissue_type="Bone marrow, chronic myelogenous leukemia"
/clone_lib="NIH_MGC_54"
/lab_host="DH10B"
/notes="Vector: pDNR-LIB"
210. .1154
/codon_start=1
/product="melanoma antigen, family A, 3"
/protein_id="AAH05963.1"
/db_xref="GI:13543627"
/translation="MPLEQRSHCKPEEGLEARGALGLVGAQAPATEEEQEAASSST
LVEVTIGVPAAESDPQSGASLPTTMYPLWSQSYEDSSNOEEGSPSTFPDLE
SEFQAALSRKVAELVHLLKYRAREPVTKAEMLGSVGNWQYFPFVIFSKASSLQLE
VFGIELMEVDPIGHLYIFATCLGLSYDGLGDNOIMPKAGLLIIVLAIAREGDCAPE
EKINELSVLEVFEGRESILGDPKLLTQHVFQENYLEYRQVPSDPAFYELWGPGR
ALVETSYVKLVHMHMKISGPHISYPPLHEWVLRGEE"
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## BASE COUNT

436 a 423 c 474 g 420 t

## ORIGIN

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Query Match 95.0%; Score 213.8; DB 9; Length 1753;
Best Local Similarity 96.9%; Pred. No. 6.7e-41;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTTCTTCTTGATCTTCAGCAAGCTTCGATTCCTTGCGAGCTGGTCTTTGGCATC 60
Db 642 TATTTCTTCTTGATCTTCAGCAAGCTTCGATTCCTTGCGAGCTGGTCTTTGGCATC 701

QY 61 GAGCTGATGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCCTGGGCCCTC 120
Db 702 GAGCTGATGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCCTGGGCCCTC 761

QY 121 TCCTAGCATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCCTGTGATAATC 180
Db 762 TCCTAGCATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCCTGTGATAATC 821

QY 181 ATCTCGGCATATTCGCAAGAGGGCGACTGTGCCCTGAGGAG 225
Db 822 GTCTGGCCATATTCGCAAGAGGGCGACTGTGCCCTGAGGAG 866
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## RESULT 15

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AR079453
LOCUS AR079453 4204 bp DNA PAT 31-AUG-2000
DEFINITION Sequence 1 from patent US 5965535.
ACCESSION AR079453
VERSION AR079453.1 GI:10006198
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4204)
AUTHORS Chaux, P., Stroobant, V., Boon-Falleur, T. and van der Bruggen, P.
TITLE Mage-3 peptides presented by HLA class II molecules
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JOURNAL Patent: US 5965535-A 1 12-OCT-1999;  
FEATURES Location/Qualifiers  
source 1..4204  
/organism="unknown"  
BASE COUNT 944 a 1144 c 1223 g 893 t  
ORIGIN

Query Match 95.0%; Score 213.8; DB 6; Length 4204;  
Best Local Similarity 96.9%; Pred. NO. 6.1e-41;  
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 1 TATTTCTTTCCTGTGATCTTCAGCAAGCTTCCGATTCCCTTCAGCTGGTCTTTGGCATC 60  
Db 2897 TATTTCTTTCCTGTGATCTTCAGCAAGCTTCCGATTCCCTTCAGCTGGTCTTTGGCATC 2956  
QY 61 GAGCTGATGGAAGTGGACCCCATCGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120  
Db 2957 GAGCTGATGGAAGTGGACCCCATCGCCACCTGTACATCTTTGCCACCTGCCTGGGCCTC 3016  
QY 121 TCCTACGATGGCCTCTCGGTGACAATCAGATCATGCCAGCAGCAGGCTTCCTGATAATC 180  
Db 3017 TCCTACGATGGCCTCTCGGTGACAATCAGATCATGCCAGCAGCAGGCTTCCTGATAATC 3076  
QY 181 ATCCTGGCCATAATCGCAAGAGAGGGGACTGTGCCCTGAGGAG 225  
Db 3077 GTCTGGCCATAATCGCAAGAGAGGGGACTGTGCCCTGAGGAG 3121

Search completed: December 4, 2001, 12:17:04  
Job time: 9082 sec